



9	942.2	56.7	2187	2	AY029215	AY029215 Lactococ
10	840.4	50.6	2834	1	AB028452	AB028452 Bacillus
11	838.8	50.5	2309	2	BACSGROSL	L10132 Bacillus st
12	822.4	49.5	2156	2	AF335323	AF335323 Listeria
13	816.4	49.2	1977	2	AF274871	AF274871 Bacillus
14	807.4	48.6	2400	2	BACGROESL	M81132 Bacillus su
15	807.4	48.6	2325	2	BACGROESL	M84965 B. subtilis
16	807.4	48.6	17516	1	AB007637	AB007637 Bacillus
17	807.4	48.1	213190	2	BSUB0004	Z99107 Bacillus su
18	799.2	47.9	2190	2	BACGROEL	D10972 Bacillus su
19	795.8	47.9	2047	2	AF259784	AF259784 Bacillus
20	786.4	47.3	296950	2	AF001508	AF001508 Bacillus
21	773	46.5	3128	1	AF010281	AF010281 Lactobac
22	771	46.4	2753	2	AF214488	AF214488 Lactobac
23	756.4	45.5	3885	2	AF269843	AF269843 Staphyloc
24	751.6	45.2	2187	3	SEU13618	U13618 Staphylococ
25	739.8	44.5	2540	2	D55630	D55630 Bacillus sp
26	726.2	44.3	2675	1	AF031929	AF031929 Lactobac
27	722.4	43.5	2712	3	STAHSP	D14711 Staphylococ
28	704.2	42.4	4710	3	LI045241	LI045241 Lawsonia in
29	688.8	41.5	3987	2	CPGROESL	X62914 C. perfringe
30	680.2	41.0	1940	1	AF080547	AF080547 Clostridi
31	674	40.6	2204	2	CPGROESL	Z68137 C. thermocel
32	673.8	40.6	1623	2	AF158449	AF159449 Clostridi
33	657	39.6	1644	2	BH078514	U78514 Bartonella
34	656.4	39.5	2103	3	TH056021	U56021 Thermotacnae
35	654.2	39.4	96109	10	AX067460	AX067460 Sequence
36	652.6	39.3	3493	2	CLOGROESLA	M74572 Clostridium
37	652.2	39.3	1644	3	ROU78515	U78515 Bartonella
38	646.4	38.9	1627	1	AF014829	AF014829 Bartonella
39	645.6	38.9	1894	2	BA08B63A	M98257 Bartonella
40	644.6	38.8	1811	3	LPNHP6G	M31918 Legionella
41	642.8	38.7	2241	3	PHA243594	AJ243594 Pseudocat
42	640.8	38.6	1635	2	BGROESL	Z15160 B. bacillifo
43	638.6	38.3	3507	2	D85628	D85628 Buchnera ap
44	636.6	38.3	34699	1	AF008210	AF008210 Buchnera
45	633.4	38.1	2715	1	AB057417	AB057417 Pseudocat

## ALIGNMENTS

RESULT 1  
AE006627/c 10389 bp DNA BCT 13-APR-2001  
LOCUS Streptococcus pyogenes strain SF370 serotype M1, section 156 of 167  
DEFINITION of the complete genome.  
ACCESSION AE006627 AE004092  
KEYWORDS AE006627.1 GI:13623059  
SOURCE Streptococcus pyogenes.  
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (bases 1 to 10389)  
Ferretti, J.J., McShan, W.M., Adjic, D., Savic, G., Lyon, K.,  
Pirneaux, C., Szate, S.S., Surov, A.N., Kenton, S., Lal, H., Lin, S.,  
Yuan, Y., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J.,  
Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.  
Complete genome sequence of an M1 strain of Streptococcus pyogenes  
Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)

TITLE JOURNAL MEDLINE  
PUBMED 11396236  
2 (bases 1 to 10389)  
Ferretti, J.J., McShan, W.M., Adjic, D., Savic, G., Lyon, K.,  
Pirneaux, C., Szate, S.S., Surov, A.N., Kenton, S., Lal, H., Lin, S.,  
Yuan, Y., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J.,  
Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.  
Direct Submission  
Submitted (10-APR-2001) Department of Microbiology and Immunology,  
University of Oklahoma Health Sciences Center, 940 St Young Blvd,  
Oklahoma City, OK 73104, USA  
Location/Qualifiers

FEATURES  
JOURNAL TITLE  
SUBMITTED (10-APR-2001) Department of Microbiology and Immunology,  
University of Oklahoma Health Sciences Center, 940 St Young Blvd,  
Oklahoma City, OK 73104, USA  
Location/Qualifiers

source  
1. 10389  
/organism="Streptococcus pyogenes"  
/strain="SF370"  
/serotype="M1"  
/db\_xref="taxon:1314"  
/complement(75..1799)  
/gene="Spy2065"  
/note="Best Blastp hit = pf112109195A chondroitin ABC  
lyase [Proteus vulgaris]"  
/codon\_start=1  
/transl\_table=11  
/product="hypothetical protein"  
/protein\_id="AAK34725.1"  
/db\_xref="GI:13623060"  
/translation="MNVLGFEPNPALIVDIIVKKNIESMGLMTKPFHHKLIKLTII  
AATSLFELIGAFYKSKHNCINATLKRASQSPFENIKALVMDINDEITDEA  
MYTFERYSQELKOKKODLKAQSDSAVYKSVGRFPIFPYRAIKPMDLTITN  
VPQADVLNOKKVAQSDSEFVKLPPTAEYASIRGKHNKRNKVKSGDGNPV  
LDLSVSPRFVTSNAKQGLDVFDDNIGTKQGLQVEDYPTTEAQAQVYKTFPQ  
ELRSOKALADVEEGATELIVTDLEEDKAGELVASAPQMLHSTGQSSNRSV  
FEGSSNAFRCIKESIKAKPOTDRKASRNISITLTMTQVCKTYYVDFTATYE  
FLDKSTDPQHTSGHINDLTGKTKAKGQHTLISQSGSKNITVAKNDQKAPSV  
FPESLGTWTGQNGLSIHMSLASDGTITTKVEQKGNRSKERTAKISKVEDKNGF  
VLTYPGSDISALVEGLGAGANKYAYGKTSKTAASVWQALTHEFDYKPLS  
GVTYKQKP"  
1962..3458  
/gene="Spy2066"  
1962..3458  
/gene="Spy2066"  
/note="Best Blastp hit = emb|CA66893.1| (X98238)  
putative; orf1 [Lactobacillus sakei]"  
/codon\_start=1  
/transl\_table=11  
/product="putative dipeptidase"  
/protein\_id="AAK34726.1"  
/db\_xref="GI:13623061"  
/translation="MINKKISAGVLSITLAFSLQSVYACTGFIIGKDLTKDQSLYG  
RTEDLEHHNKNFIVRIKONAPAGEKKKDLNNGPEYLPDEHSRYSAIPDPKRGY  
DEAGFNEFCVMSATVYASANDAIQIDPYVKNGLAESMTSVIIPSKTAREGVALI  
AKYTERGAENISYVTLADKQINYMELSGHOYAIKPPDKYVAFPPYTLHYDF  
NDEKNTIASDEYKAKKAKSTEDKQFLKASYNPPLDARKSSTSGISLDPQS  
KVYKDSNTELLQSTDKLEDAKLDQRNFBELDKPLDDQALDQKRSKAAK  
GYAVPISNPNVMEAHIFQKDKDIPAELEGVWMLSSIPRAAPLYALNLSRTYEAQ  
EKSTQYNDKSWYVSHINDVAAHPKPFQGVYIDEMKGLERTYIAEDQKSTKESIDL  
VSDPKRAOEDKADISLDRAEKTRFKAIKALVKEKPKNKKGLNRS"  
complement(4661..6292)  
/gene="groEL"  
/note="Spy2070"  
complement(4661..6292)  
/gene="groEL"  
/note="The N-terminal amino acid sequence of this ORF has  
been determined from a spot isolated by 2-D gel  
electrophoresis from another strain of S. pyogenes. Hogan,  
D. A., Whitton, M. M., Rogers, J. and R. A. Vanhogen.  
2000. Two-dimensional gel electrophoresis map of  
Streptococcus pyogenes proteins. Unpublished data.; Best  
Blastp hit = emb|CA61520.1| (X89236) heat shock protein  
[Streptococcus pyogenes]"  
/codon\_start=1  
/transl\_table=11  
/product="heat shock protein (chaperonin)"  
/protein\_id="AAK34727.1"  
/db\_xref="GI:13623062"  
/translation="NAKDIFSASARAAMVGVMDIADTVKTLGPKGRNVLEKAG  
SPITNDGVTIAKEILEDHPENNGALVSEVASKINDIAGDGTATVLAQVAVHG  
LKHTVAGNDPIGRGIFTATATVVALKAIQAPVSGKRAINOVAAVSREKGEYI  
SEAMERVGVGVITPEPCKMETELPVEGMDPDRYLSQVYTNKEMVADLNPPI  
LITDKVSNIDQILPLDEYVLTNRPLIITADVDDEALPTLVKRTGNTVAVKA  
PQGDNRKAMEDIALILGVVITVEDLQKATVATVLAQVAKITVQKSTVAVES  
GSSEAIANRIALIKSQLETTSDPDKREKLDIERAKLAGVAVAKGATETALKEMRL  
RIDBALNATRAAVEGIVAGGATLITVIEKVALELEDGATGNIVLRALDEPVRQ

gene  
 IALNAGEGVYIDKLNKSPAGTGNAATGEMVDMITKGTIDPVKVTSAIONASVA  
 SLITTEAVANKPPAPAPAMPAGNDPGMKGF  
 complement(6328. .6618)  
 /gene="groes"  
 /note="SPY2072"  
 complement(6328. .6618)  
 /gene="groes"  
 /note="The N-terminal amino acid sequence of this ORF has  
 been determined from a spot isolated by 2-D gel  
 electrophoresis from another strain of S. pyogenes. Hogan,  
 D. A., Whitton, M. W., Rogers, J. and R. A. Vanhogen.  
 2000. Two-dimensional gel electrophoresis map of  
 Streptococcus pyogenes proteins. Unpublished data.; Best  
 Blastp hit = gb|AA75592.1|AF214488\_2 (AF214488) GROES  
 [lactobacillus johnsonii]"  
 /codon\_start=1  
 /transl\_table=11  
 /product="heat shock protein - co-chaperonin"  
 /protein\_id="AAK34728.1"  
 /db\_xref="GI:13623063"  
 /translation="MLKPLGDRVVRPDEKEQVGVGLAGTHKESTKATVLA  
 TGVKITDSDVLPSSVGOEVLVENGHDEVTVDDEKVSIIRESDIIVTK"  
 complement(6796. .9240)  
 /gene="clpc"  
 /note="SPY2073"  
 complement(6796. .9240)  
 /gene="clpc"  
 /note="Best Blastp hit = gb|AAC44446.1| (U40604) CLPC  
 klpase [Listeria monocytogenes]"  
 /codon\_start=1  
 /transl\_table=11  
 /product="putative endopeptidase Clp APP-binding chain C"  
 /protein\_id="AAK34729.1"  
 /db\_xref="GI:13623064"  
 /translation="MIMSTRMODIFRHOAFQFARPDSCLETHWVILLAMAVVNSIA  
 NMLISEYDAOVAIEEYPAALIAMKTRKQQLSRVDFRQSTLTINLAFKQASIT  
 RQEVGSEHYVFAILLNPDIAMSLKLEIASTQIKDNGNPPALADLRVAIRHAGYSK  
 EYKAIHELKRPKTKTOGTFSDMKRPSFAGLSLFTDLIEMARQELLEVSIGRQ  
 EYKSMIOVLSKRTKNPVLVDAGVGTALAGVLPALANGAIPLEKMEVLELDLM  
 SYVAGTRGRDGEERMOQIIDIEADQIILFVDELITMGSGIDSTIDANAILRP  
 AASRGLTHMGVATQOEYOKHIEKDAISRFAKILIEEPNTDAYOILMLKLSYET  
 YHNSISNEAVATVKAHARLYTSKNLPDSALIDLEASAVONNVKSAEETLPTD  
 QALLINGDKKYSRLAKKAGKMRKPTVEDIILATLSKSGTLEKLNQADSKYL  
 NLEKLHRRVIGODAAVATSAIRRQSGIRGRKPSSEFELPTGVGTIELAKL  
 AYLVDDEALAIRFDMSERMEKFRASRLNKAAPGVIGDEGELQKRNKPSVLEF  
 DEYEAHPDITFNVLDVLDGILDSGRKVPSTNIIIMTNSLGAIALRDKTVFG  
 VNDIQHQAEMERILELKRTPERFINRIDEKVFHSLTODNARDVVKIMVPLIT  
 TLAEGILKIQPLALNHLSEVGYDEHMGARPLRLTQETEDKLSLEILSRELSGH  
 TKIGLSHGKLTFFHA"  
 complement(9240. .9701)  
 /gene="ctsr"  
 /note="SPY2074"  
 complement(9240. .9701)  
 /gene="ctsr"  
 /note="Best Blastp hit = sp|P37568|CTSR\_BACSU  
 TRANSCRIPTIONAL REGULATOR CTSR >g12127052|P1R1S66112  
 transcription repressor ctsr - Bacillus subtilis  
 >g1467471|dbj|BAA05317.1| (D26185) unknown [Bacillus  
 subtilis] >g12632350|emb|CA81859.1| (Z29104)  
 transcriptional regulator [Bacillus subtilis]"  
 /codon\_start=1  
 /transl\_table=11  
 /product="putative transcriptional regulator"  
 /protein\_id="AAK34730.1"  
 /db\_xref="GI:13623065"  
 /translation="MPKNTSDSIEEYINELAKSGIAIKRSLADSFQVVSQIN  
 YTKPFTESRGYEVESKGGGYIRAKVHFDHLLGNLMATIEDCISQVFTDSI  
 QILFPEHLIREGNIILAAVSDVGTGDSITRARMYRLQRIKRGNS"  
 complement(9897. .10100)  
 /gene="csp"  
 /note="SPY2077"  
 complement(9897. .10100)  
 /gene="csp"

Query Match 97.7% Score 1622.2; DB 1; Length 10389;  
 Best Local Similarity 99.8% Pred. No. 0;  
 Matches 1624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ORIGIN  
 BASE COUNT 3077 a 2210 c 1855 g 3247 t  
 OXKAEVEGGRGPOVAVNITKLA  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623066"  
 /protein\_id="AAK34731.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34732.1"  
 /db\_xref="GI:13623067"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623068"  
 /protein\_id="AAK34733.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34734.1"  
 /db\_xref="GI:13623069"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623070"  
 /protein\_id="AAK34735.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34736.1"  
 /db\_xref="GI:13623071"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623072"  
 /protein\_id="AAK34737.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34738.1"  
 /db\_xref="GI:13623073"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623074"  
 /protein\_id="AAK34739.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34740.1"  
 /db\_xref="GI:13623075"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623076"  
 /protein\_id="AAK34741.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34742.1"  
 /db\_xref="GI:13623077"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623078"  
 /protein\_id="AAK34743.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34744.1"  
 /db\_xref="GI:13623079"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623080"  
 /protein\_id="AAK34745.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34746.1"  
 /db\_xref="GI:13623081"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623082"  
 /protein\_id="AAK34747.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34748.1"  
 /db\_xref="GI:13623083"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623084"  
 /protein\_id="AAK34749.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34750.1"  
 /db\_xref="GI:13623085"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623086"  
 /protein\_id="AAK34751.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34752.1"  
 /db\_xref="GI:13623087"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623088"  
 /protein\_id="AAK34753.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34754.1"  
 /db\_xref="GI:13623089"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623090"  
 /protein\_id="AAK34755.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34756.1"  
 /db\_xref="GI:13623091"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623092"  
 /protein\_id="AAK34757.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34758.1"  
 /db\_xref="GI:13623093"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623094"  
 /protein\_id="AAK34759.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34760.1"  
 /db\_xref="GI:13623095"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623096"  
 /protein\_id="AAK34761.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34762.1"  
 /db\_xref="GI:13623097"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623098"  
 /protein\_id="AAK34763.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34764.1"  
 /db\_xref="GI:13623099"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623100"  
 /protein\_id="AAK34765.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34766.1"  
 /db\_xref="GI:13623101"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623102"  
 /protein\_id="AAK34767.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34768.1"  
 /db\_xref="GI:13623103"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623104"  
 /protein\_id="AAK34769.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34770.1"  
 /db\_xref="GI:13623105"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623106"  
 /protein\_id="AAK34771.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34772.1"  
 /db\_xref="GI:13623107"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623108"  
 /protein\_id="AAK34773.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34774.1"  
 /db\_xref="GI:13623109"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623110"  
 /protein\_id="AAK34775.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34776.1"  
 /db\_xref="GI:13623111"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623112"  
 /protein\_id="AAK34777.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34778.1"  
 /db\_xref="GI:13623113"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623114"  
 /protein\_id="AAK34779.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34780.1"  
 /db\_xref="GI:13623115"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623116"  
 /protein\_id="AAK34781.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34782.1"  
 /db\_xref="GI:13623117"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623118"  
 /protein\_id="AAK34783.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34784.1"  
 /db\_xref="GI:13623119"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623120"  
 /protein\_id="AAK34785.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34786.1"  
 /db\_xref="GI:13623121"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623122"  
 /protein\_id="AAK34787.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34788.1"  
 /db\_xref="GI:13623123"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623124"  
 /protein\_id="AAK34789.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34790.1"  
 /db\_xref="GI:13623125"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623126"  
 /protein\_id="AAK34791.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34792.1"  
 /db\_xref="GI:13623127"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623128"  
 /protein\_id="AAK34793.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34794.1"  
 /db\_xref="GI:13623129"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623130"  
 /protein\_id="AAK34795.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34796.1"  
 /db\_xref="GI:13623131"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623132"  
 /protein\_id="AAK34797.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34798.1"  
 /db\_xref="GI:13623133"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623134"  
 /protein\_id="AAK34799.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34800.1"  
 /db\_xref="GI:13623135"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623136"  
 /protein\_id="AAK34801.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34802.1"  
 /db\_xref="GI:13623137"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623138"  
 /protein\_id="AAK34803.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34804.1"  
 /db\_xref="GI:13623139"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623140"  
 /protein\_id="AAK34805.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34806.1"  
 /db\_xref="GI:13623141"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623142"  
 /protein\_id="AAK34807.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34808.1"  
 /db\_xref="GI:13623143"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623144"  
 /protein\_id="AAK34809.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34810.1"  
 /db\_xref="GI:13623145"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623146"  
 /protein\_id="AAK34811.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34812.1"  
 /db\_xref="GI:13623147"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623148"  
 /protein\_id="AAK34813.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34814.1"  
 /db\_xref="GI:13623149"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623150"  
 /protein\_id="AAK34815.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34816.1"  
 /db\_xref="GI:13623151"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623152"  
 /protein\_id="AAK34817.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34818.1"  
 /db\_xref="GI:13623153"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623154"  
 /protein\_id="AAK34819.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34820.1"  
 /db\_xref="GI:13623155"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623156"  
 /protein\_id="AAK34821.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34822.1"  
 /db\_xref="GI:13623157"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623158"  
 /protein\_id="AAK34823.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34824.1"  
 /db\_xref="GI:13623159"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623160"  
 /protein\_id="AAK34825.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34826.1"  
 /db\_xref="GI:13623161"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623162"  
 /protein\_id="AAK34827.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34828.1"  
 /db\_xref="GI:13623163"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623164"  
 /protein\_id="AAK34829.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|CA76697.1| (Y17216) cold  
 shock protein D [Lactococcus lactis]"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="AAK34830.1"  
 /db\_xref="GI:13623165"  
 /translation="MAQGYKMFNAEKGRFISTENGODVFAHPSAIONGFTEEG  
 /db\_xref="GI:13623166"  
 /protein\_id="AAK34831.1"  
 /product="putative cold shock protein"  
 /transl\_table=11  
 /codon\_start=1  
 /note="Best Blastp hit = emb|

RESULT,	2
SPGROELGN	
LOCUS	SPGROELGN 2683 bp DNA ECT 26-SEP-1997
DEFINITION	S. pyogenes DNA for groEL gene.
ACCESSION	X89336
VERSION	X89236.1 GI:2462691
KEYWORDS	groEL gene; heat shock protein 60 (GroEL) like protein.
SOURCE	Streptococcus pyogenes.
ORGANISM	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae Streptococcus.
REFERENCE	Podbielski, A. 1 (bases 1 to 2683)
AUTHORS	Podbielski, A.
TITLE	Direct Submission
JOURNAL	Submitted (29-JUN-1995) A. Podbielski, Institut f Med Mikrobiologie, an der Rhein Westf. Techn. Hochschule, Aachen,

```

gene      /organism="Streptococcus pyogenes"
          /strain="serotype M49"
          /isolate="C5101"
          /db_xref="taxon:1314"
1..1446
/gene="groEL"
CDS
<1..1446

```

Query Match	85.18;	Score 1413.4;	DB 3;	Length 2683;
Best Local Similarity	98.98;	Pred. No. 1.7e-273;		
Matches 1423; Conservative	0;	Mismatches 16;	Indels 0;	Gaps 0

QY	201	GATCATTTTGAANAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTCTAAACCAATGAT	26
Db	1	GATCATTTTCCAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTCTAAACCAATGAT	60
QY	261	ATTGGTGGTATGGGACGACTACTGCAACAGTTTTGACACAAAGCCATTGTTCTAGAGA	320
Db	61	ATTGGTGGTATGGGACGACTACTGCAACAGTTTTGACACAAAGCCATTGTTCTAGAGA	120
QY	321	CTAAAAAATGTGACAGCAGGTGCTATATCCAAATGGTATCCGTCAGAGCATTTGAACAGA	380
Db	121	CTAAAAAATGTGACAGCAGGTGCTATATCCAAATGGTATCCGTCAGAGCATTTGAACAGA	180
QY	381	ACAGCAACACCTTTTGAAGCCCTGAAGCCATTGTCMAACCTGTAATGTGGCAAGAACCT	440
Db	181	ACAGCAACACCTTTTGAAGCCCTGAAGCCATTGTCMAACCTGTAATGTGGCAAGAACCT	240
QY	441	ATTGCTAGGTGGCTGACATATCATACAGCTGTGAANAAGTTGAGAGATATCTACAGA	500
Db	241	ATTGCTAGGTGGCTGACATATCATACAGCTGTGAANAAGTTGAGAGATATCTACAGA	300
QY	501	GCTATGAGGCGTGTGGGACAGATGTGTGATTACCATCGAAGAAATTCAGAGTATGAA	560
Db	301	GCTATGAGGCGTGTGGGACAGATGTGTGATTACCATCGAAGAAATTCAGAGTATGAA	360
QY	561	ACAAACATTGAAGTGGTGAAGGCAATGCAATTGACCGTGGTTACCGTCTCAATACATG	620
Db	361	ACAAACATTGAAGTGGTGAAGGCAATGCAATTGACCGTGGTTACCGTCTCAATACATG	420
QY	621	GTCAGAGCAATGAAAAAATGGTTCGACAGACTTTGAAAAACCCATTATCTTAATACCGAT	680
Db	421	GTCAGAGCAATGAAAAAATGGTTCGACAGACTTTGAAAAACCCATTATCTTAATATGAT	480
QY	681	AAAAAAGTCAACATCCAAAGACATTTTGGCACACTACTTGTAGAGAGTTCTTAAACCAAC	740

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1	Jwo-Farn, C.	Cloning, sequencing, and characterization of 60 kDa Chaperon from <i>Streptococcus agalactiae</i> unpublished	2 (bases 1 to 1718)	2	Jwo-Farn, C.	Direct Submission Submitted (30-NOV-2000) Department of Microbiology, National Tain University, Jen-Ai Rd. section 1, No. 1, Taipei, Taiwan 10018, Republic of China	Location/Qualifiers
1.1718							
/organism="Streptococcus agalactiae"							
/db_xref="taxon:1311"							
96..1718							
/note="prevents misfolding; promotes refolding and proper assembly of unfolded polypeptides generated under stress conditions; forms 14-subunit oligomer composed of two 7-subunit stacked rings; belongs to the Hsp60 chaperonin family"							
/codon_start=1							
/transl_table=1							
/product="60kda chaperonin"							
/protein_id="AAK12938.1"							
/db_xref="GI:13123671"							
/translation="MARDIKFSADARSAMVRGVDLADPVTPLGKRNVLLEKAGFGLPIVNDGVTIAKEIELEDFHEFNMGAKLVEASVSTNDIDGTTTAAVLPDAIVRGRLKAVTANPGIIRAGIEETVSAVAEELKIAQPSYSEKIAIAOVAASRSSEKVEEYI SEMEAVGSDVITIEESRCMTELEVEGMOFPGYLSQNTDDEKNSLEMPYI LIDDKISNIOEILPLLEEVLKTNRPILIIADVDGALPTLVLRIGTFENVAAVLA PGEDGSRKMLIEDAIIITGCTVTEDELGLDKATMVOIGSAAKVVVDSDIVIEGDA SDAIRNARVAIISOMEATSDPDEKLOERLAKLAGVAIVKGAATELEKMKI RIEDLNTAIVRAIEGIVSGSGFALNTVIEKVAALIKNGDEETGRNIVIRALEEPVQ IANNGYGSVITIAAREKISQSGIFGFMANGEVMDVTTGIIIDPVKTRALONASAVVA SLITTEAVANKEPREPAPNAMPDSMKGG"							
BASE COUNT	531 a	279 c	408 g	500 t			
ORIGIN							
Query Match	63.4%	Score 1053.8;	DB 2;	Length 1718;			
Best Local Similarity	78.9%;	Pred. No. 2.1e-201;					
Matches 1269;	Conservative	0;	Mismatches 337;	Indels	3;	Gaps	1;
QY	14	TATGGCAAGAAMATCAAAATTTTCACGAGTGGCCCGCTCGCTGCAATGGTGGCCGAGTGTGA	73				
DB	95	TATGGCAAGAAMATTTAAATTTTCACGAGTGGCCCGCTCGCAATGGTGGCCGAGTGTGA	154				
QY	74	TATGTTAGCAGATACCGTCMAAGTACCCCTTGCTCTTAAAGGCGCAATGTTGTTCTTGA	133				
DB	155	TATTTTACGTATACAGTCTTTGTAACTTATAGTGCCCTAAAGGCGCTAATGTTGTTCTTGA	214				
QY	134	AAACACTTTCGTTCCCTTAAATACAAAGACGGGGATACCATTTGCTTAAAGAGATCGA	193				
DB	215	AAAACATTCGTTCTTCCTTATTAACAAAGATGGGTATACCATTTGCTTAAAGAGATCGA	274				
QY	194	ATTGAGAGATCATTTTGGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTTAAAC	253				
DB	275	GCTAAGAAATCATCTTTGAAAATAATTTGGAGCTAAACTTGTGTGAGAAAGGCTTTAAAC	334				
QY	254	CAATATATTCCTGCTGATGGGACACACTACCTACGACAGTGTGTGACACAGCATTTGTCA	313				
DB	335	TATATATATTCCTGCTGATGGGACACACTACCTACGATTTGTGACCATTTATTTGACG	394				
QY	314	TGAAGAGATTAATAAATGTGACAGCGAGGTCAATCAATTTGGATATTCGTCGAGGACATTA	373				
DB	395	GGAAGCTTTAAATATGTACGTACGAGGGGCAATTCGATTTGGCATTTCTCTGATATGA	454				
QY	374	AACAGCAACACACAGCTGTGAAGCCTTGAAGACATTTGCTCAACTGTATCTGGCAA	433				
DB	455	AACAGCTGTTCCTGCTGATGGGACACACTACCTAAAGAGATTTGACACAGTTCGAGCAA	514				

```

OY 434 GGAAGCTATGCTCAGGTCGCTCAGTATCATCAGCTCTGAAAGGTTGGAGATAT 493
    |||||
DB 515 AGAAGCTATGCTCAGTATGCTCAGTATGCTCAGTATGCTCAGTATGCTCAGTAT 574
    |||||
OY 494 CTCAGAGCTATGAGGCTGAGGCAACATGCTGATTCACATGCAAGATCTGAGG 553
    |||||
DB 575 TCTGAGAGCTATGAGGCTGAGGCAACATGCTGATTCACATGCAAGATCTGAGG 634
    |||||
OY 554 TATGAAACAGAGCTATGAGGCTGAGGCAACATGCTGATTCACATGCTGATTC 613
    |||||
DB 635 TATGAAACAGAGCTATGAGGCTGAGGCAACATGCTGATTCACATGCTGATTC 694
    |||||
OY 614 ATACATGCTCAGACATGAAAGATGCTGCAAGCTGCAAGATGCTGCAAGATGCT 673
    |||||
DB 695 GATATGCTCAGACATGAAAGATGCTGCAAGCTGCAAGATGCTGCAAGATGCT 754
    |||||
OY 674 CAGGATGAAAGATGCTGCAAGATGCTGCAAGCTGCAAGATGCTGCAAGATGCT 733
    |||||
DB 755 TACAGATGAAAGATGCTGCAAGATGCTGCAAGCTGCAAGATGCTGCAAGATGCT 814
    |||||
OY 734 AACCAACGCTCATCTACTCATTTATGAGATGATGAGTGGAGGCACTTCCAACTT 793
    |||||
DB 815 AACCAACGCTCATCTACTCATTTATGAGATGATGAGTGGAGGCACTTCCAACTT 874
    |||||
OY 794 TGTCTGAAACAGATGCTGAGTATCTTCATGCTGCTGCTGCTGCTGCTGCTGCT 853
    |||||
DB 875 TGTCTGAAACAGATGCTGAGTATCTTCATGCTGCTGCTGCTGCTGCTGCTGCT 934
    |||||
OY 854 TGATGCTGTAAGCTATGCTGTAAGATGCTATGCTGTAAGATGCTATGCTGTAAG 913
    |||||
DB 935 TGATGCTGTAAGCTATGCTGTAAGATGCTATGCTGTAAGATGCTATGCTGTAAG 994
    |||||
OY 914 AGAGATCTGAGACTGTAATTAAGATGCTATGCAATGAGCCCTTGGACAGCTGCT 973
    |||||
DB 995 TGAAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
    |||||
OY 974 GATTACAGTATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1033
    |||||
DB 1055 AGTAAACAGTATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1114
    |||||
OY 1034 TGTACACGCTATGCTATGATTAAGATGATGATGATGATGATGATGATGATGAT 1093
    |||||
DB 1115 TGTACACGCTATGCTATGATTAAGATGATGATGATGATGATGATGATGATGAT 1174
    |||||
OY 1094 TGAAGAACTACAGAACTGCTTGGCAATTAAGTGTGCTGCTGCTGCTGCTGCTG 1153
    |||||
DB 1175 TGAAGAACTACAGAACTGCTTGGCAATTAAGTGTGCTGCTGCTGCTGCTGCTG 1234
    |||||
OY 1154 AGTCAACAGAGAGAGCTTTAAAGAAAGAACTTCCATGAGAGTCTTAATTC 1213
    |||||
DB 1235 TGCAGCACTGAAACAGAAATTAAGAGATGAACTTCCATGAGAGTCTTAATTC 1294
    |||||
OY 1214 TACACGCTGACGCTTGAAGAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1273
    |||||
DB 1295 AACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
    |||||
OY 1274 TATGAAAGATGAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCT 1333
    |||||
DB 1355 TATGAAAGATGAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGCT 1414
    |||||
OY 1334 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1393
    |||||
DB 1415 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1474
    |||||
OY 1394 CGTAGTATGAGCAAGTGAAGAAACAGCCCTGAGAGAGAGATTAATGCTGAGAG 1453
    |||||
DB 1475 AGTATATGAGCAAGTGAAGAAACAGCCCTGAGAGAGAGATTAATGCTGAGAG 1534
    |||||
OY 1454 TGAAGTATGAGCAAGTGAAGAAACAGCCCTGAGAGAGAGATTAATGCTGAGAG 1513
    |||||
DB 1535 AGATGAGTATGAGCAAGTGAAGAAACAGCCCTGAGAGAGAGATTAATGCTGAGAG 1594
    |||||

```

```

OY 1514 GCTTCAAAATGACAGCTTCTGCTAGCTATGCTTATTTGACACAGAGAGCTTGTCTAA 1573
    |||||
DB 1595 ACTTCAAAATGACAGCTTCTGCTAGCTATGCTTATTTGACACAGAGAGCTTGTCTAA 1654
    |||||
OY 1574 TAAACCTGAAAC--AGCTACGACGCGCCAGCAATGCCAGGATG 1619
    |||||
DB 1655 TAAACCTGAAACAGAGCTCTACAGCTCTGCAATGATGATCATCTATG 1703
    |||||

RESULT 4
SPNEU1924/c
LOCUS SPNEU1924 21494 bp DNA HTG 16-DEC-2000
DEFINITION Streptococcus pneumoniae clone G54, *** SEQUENCING IN PROGRESS ***
ACCESSION AL449946
VERSION AL449946.1 GI:11545171
KEYWORDS HTG; HTGS; PHASE2.
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 21494)
AUTHORS Dopazo, J., Mendoza, A., Herrero, J., Caldera, F., Pollasi, A.,
Humbert, Y., Friedl, L., Guerrier, M., Grand-Schenck, E., Gandin, C., de
Garcia-Bustos, J.F.
TITLE Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A.,
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
COMMENT * NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1..21494
location/Qualifiers
/organism="Streptococcus pneumoniae"
/serotype="19F"
/db_xref="taxon:1313"
/clone="G54"
BASE COUNT 6466 a 4646 c 3734 g 6638 t 10 others
ORIGIN

Query Match 62.5% Score 1038 6: DB 84: Length 21494,
Best local similarity 77.5% Pred. No. 1.8e-199,
Matches 1257; Conservative 0; Mismatches 364; Indels 0; Gaps 0:

OY 14 TATGCAAAAGCAATTCATTTTCAGCAGATGCGCTGCTGCTGCTGCTGCTGCTG 73
    |||||
DB 8015 TATGCAAAAGCAATTCATTTTCATCAGATGCCGCTGCTGCTGCTGCTGCTGCTG 7956
    |||||
OY 74 TATGTTACAGATACCGTCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 133
    |||||
DB 7955 TATTTCTGCAACACTGTTAAAGTAACTTGGACCAAAAGTGCACATGCTGCTGCTG 7896
    |||||
OY 134 AAAAGCTTTTGTCTCCCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 193
    |||||
DB 7895 AAAGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7836
    |||||
OY 194 ATTAGAGATCATTTTGAAGAAATGAGGCAAAATTTGCTGCTGCTGCTGCTGCTGCT 253
    |||||
DB 7835 ATTGGAAGACCATTTTGAAGAAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7776
    |||||
OY 254 CAATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
    |||||
DB 7775 CAATATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7716
    |||||
OY 314 TGAAGACTAAAGATGTAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
    |||||
DB 7715 TGAAGACTAAAGATGTAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7656
    |||||
OY 374 AACAGCAAGCAAGAGCTGTTAAAGCTTGAAGACCTTCTTAACCTGATCTGCAAA 433
    |||||

```

Db 7655 AACGACGTTGCCGACGAGTGAAGCTTTGAAAAACACGCCATCCCTGTTGCCAATA 7356

Qy 434 GGAAGCTATTGCTCAGGTGCTGCTCAGTATCATCTCAGCTCTGAAAAAGTTGGAGAGTAT 493

Db 7595 AGAAGCTATGCTCAAGTGTGACCGGTATCTCTCTGTTGAAAAAGTTGGTGTACAT 7336

Qy 494 CTCGAAAGCTATGAGCGGTGGGCAAGGATGATGATGATGATGATGATGATGATGATGAT 553

Db 7335 CTCGAAAGCTATGAGCGGTGGGCAAGGATGATGATGATGATGATGATGATGATGATGAT 7476

Qy 554 TATGAAAGAGAACTGAAGTGTGTAAGGCTGCAATTTGACCGTGTGTTACCTGTCTCA 613

Db 7475 TATGAAAGAGAACTGAAGTGTGTAAGGCTGCAATTTGACCGTGTGTTACCTGTCTCA 7416

Qy 614 ATTCATGCTGACGACATGAAAAAATGGTTGCGACCTGAAACCCCTTATCTAT 673

Db 7415 GTACATGCTGACGACATGAAAAAATGGTTGCGACCTGAAACCCCTTATCTAT 7336

Qy 674 CACGATAAAAAAGTGTCAAAACATCAAGACATTTTGCCTACTTGAAGAAATTTCTTA 733

Db 7355 TACAGACAAAAAATTTCCCAATATCCAAAGAAATCTTCCACTTTTGAAGACATCTCCA 7296

Qy 734 AACCAACCGCTTACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793

Db 7295 AACCAATCGCTTACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7236

Qy 794 TGTCTTGAACAAAGATTTCTGCTGATCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 853

Db 7235 TGTCTTGAACAAAGATTTCTGCTGATCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 7176

Qy 854 TGATCGTCTAAAGCTATGCTGTAAGACATGCTATCTTCAAGTGTGCTGCTGCTGCTGCTGCT 913

Db 7175 TGACCTGCTCAAGCAAGCATGCTTGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7116

Qy 914 AGAGATCTAGACATGATTTAAAGATGCTCAATGACAGCCCTTGGACGCTGCTGCTGCT 973

Db 7115 AGAGATCTAGACATGATTTAAAGATGCTCAATGACAGCCCTTGGACGCTGCTGCTGCTGCT 7056

Qy 974 GATTACGTTGATTAAGATAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033

Db 7055 AGTACCGCTGACCAAGCATGCTTGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6996

Qy 1034 TGTACCGCTTATGACATGATTTAAAGATGCTCAATGACAGCCCTTGGACGCTGCTGCTGCT 1093

Db 6995 TGTACCGCTTATGACATGATTTAAAGATGCTCAATGACAGCCCTTGGACGCTGCTGCTGCT 6936

Qy 1094 TGAAGAACTACAGAGCTTTGCGAAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1153

Db 6935 TGAAGAACTACAGAGCTTTGCGAAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6876

Qy 1154 AGCTCAAGAGAGAGCTTTAAAGAAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213

Db 6875 AGCTCAAGAGAGAGCTTTAAAGAAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6816

Qy 1214 TACAGCTGACCGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1273

Db 6815 TACTCTGACCGCTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6756

Qy 1274 TATTGAAAGAGAGAGCTTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1333

Db 6755 GATTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6696

Qy 1334 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1393

Db 6695 TCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6636

Qy 1394 CGTAGTATTGACAGAGCTTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1453

Db 6635 TATCGTATTGACAGAGCTTTGAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6576

Qy 1454 TGAGTGGGTTGATGATTTAAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1513

Db 6575 CGAGTGGGTTGATGATTTAAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6516

Qy 1514 GCTTCAAAATGACAGCTTCTGATGCTACTTATTTTGAACAGAGACAGTGTGCTA 1

Db 6515 CTTACAAATGACAGCTTCTGATGCTACTTATTTTGAACAGAGACAGTGTGCTA 1

Qy 1574 TAAACCTGAAAGCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1

Db 6455 TAAACCTGAAAGCTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 639

Qy 1634 G 1634

Db 6395 G 6395

RESULT 5

AX073958 1926 bp DNA PAT 06-FEB-2001

LOCUS AX073958

DEFINITION Sequence 50 from Patent WO0104344.

ACCESSION AX073958

VERSION AX073958.1 GI:12710218

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

artificial sequence.

REFERENCE

1 (bases 1 to 1926)

AUTHORS Siegel, M., Chu, N.R. and Mizzen, L.A.

TITLE Induction of a Th1-like response in vitro

Journal Patent: WO 0104344-A 50 18-JAN-2001;

Stressgen Biotechnologies Corporation (CA)

Location/Qualifiers

1..1926

source

1..1926

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="fusion sequence"

1..1926

/note="unnamed protein product"

/codon\_start=1

/transl\_table=11

/protein\_id="CAC28432.1"

/db\_xref="GI:12710219"

/translation="MAKESFSSDARSAMVGVLDIADYKVTIAPKGRNVLEKSG

SPITNDGVTIAKETIEDHDPENMGAKLYSPVASKTDYDIAGCTTATATVLAIVREI

IKNTTAAANDIGIRICETETNAVAAYEALKNNVITPAKREIAQVAAYVSRSEKGEYI

SEAMEKVDVITIESEKMELEVEGMDPFGTLISQHWYDSEKVADELNPIT

LITRKIKSNIOELPLESIILOSNPILLIADVDGSALEPLVUNKIRGTENVVAVA

PGFEDRRKMLEDIATLNGVITFEDLGLDKATTEALGOAARVYVDKDSVIVEGA

GNPEAISHRAVAVIKSQIETTTSEPDREKLOERLAKLSGVAIVKGAATELEKML

RIEDALNATRAVEEGIVAGGATLANIYPAVATLELIGDEAGRIYVLALEEVQ

IAHNAEGSVIVDRKNAELIGENATGEVMYIDOGIIPDKVSRALONASVA

SLITTEAVVANKPEPVAPAMPDPSMMGGMGMSMHDGPTLHEHMDLPDPTDLY

CYEDLNSSEDEIDGPAQGAEPBRAHYNIYVTCCKDSLRLCYGSTRHNDIRLED

LMQTDIVICPICORP"

BASE COUNT 585 a 382 c 464 g 495 t

ORIGIN

Query Match 62.5%; Score 1038.4; DB 10; Length 1926;

Best Local Similarity 77.5%; Pred. No. 2.6e-198;

Matches 1288; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

Qy 15 ATGGCAAAAGAAATTAATTTTTCAGCAGATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 74

Db 1 ATGGCAAAAGAAATTAATTTTTCAGCAGATGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60

Qy 75 ATGTTCGACATACCGCTCAAGATTAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 134

Db 61 ATCTTCGACATACCGCTCAAGATTAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Qy 135 AAAGCTTTGCTTCCCTTAATTAAGAGAGCGGCTGACATGCTGCTGCTGCTGCTGCTGCTGCT 194

Db 121 AAGTCAATTCGCTTACCTTGATTAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

Qy 195 TTAGAAAGATCATTTGAAAGATGAGAGCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254

```

181 TTGAGAGACACATTTTGAATAATGGGTGCCAATGTGATCAGAAAGCTTCAAAACC 240
OY 255 AATGATATTCGTGATGATGGAGACATACGACAGAGTTTGGACACAGCATTTGCT 314
Db 241 AATGATATTCGTGATGATGGAGACATACGACAGAGTTTGGACACAGCATTTGCT 300
OY 315 GAAGACCTAAAAATGTGACAGAGGTGCTAATCCAAATGTGATCCGTGAGGCATTTGA 374
Db 301 GAAGACCTAAAAATGTGACAGAGGTGCTAATCCAAATGTGATCCGTGAGGCATTTGA 360
OY 375 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAGCATTGCTCAACCTGATCTGCAAG 434
Db 361 ACAGCAAGTTGGCGAGCAGAGTTGAAGCTTTGAAAAACACGATCCTCTGTGCAATTA 420
OY 435 GAAGCTATTCGTGATGATGGAGACATACGCTTGAAGAGTTTGGAGAGTATATC 494
Db 421 GAAGCTATTCGTGATGATGGAGACATACGCTTGAAGAGTTTGGAGAGTATATC 480
OY 495 TCAGAACCTATGAGCGGTGGGCAACGATGGTGTGATTAACATCGAAGATCGAGGT 554
Db 481 TCAGAACCTATGAGCGGTGGGCAACGATGGTGTGATTAACATCGAAGATCGAGGT 540
OY 555 ATGGAACAGACACTGAAGTGTGAGGATGCAATTTGACCGTGTACCTGTCTCAA 614
Db 541 ATGGAACAGACACTGAAGTGTGAGGATGCAATTTGACCGTGTACCTGTCTCAA 600
OY 615 TACATGCTCACAGACATGAAAAATGGTTGGACAGCTTGAACCACTTATCTTAATC 674
Db 601 TACATGCTCACAGACATGAAAAATGGTTGGACAGCTTGAACCACTTATCTTAATC 660
OY 675 ACGGATAAAAAGTGCACAAACATCCACAGCATTTTGGCAGTCTACTGAGAGTTTAA 734
Db 661 ACGGATAAAAAGTGCACAAACATCCACAGCATTTTGGCAGTCTACTGAGAGTTTAA 720
OY 735 ACCAACCGTCCATTAATCTATATGCAATGATGTGATGATGATGATGATGATGATG 794
Db 721 ACGAACCGTCCATTAATCTATATGCAATGATGTGATGATGATGATGATGATGATG 780
OY 795 GCTTGAACAAAGATGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
Db 781 GCTTGAACAAAGATGCTGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
OY 855 GATGCTGTAAGCTATGCTTGAAGACATCTGATCTTGAAGAGTGTGACAGTATTA 914
Db 841 GATGCTGTAAGCTATGCTTGAAGACATCTGATCTTGAAGAGTGTGACAGTATTA 900
OY 915 GAGGATCTAGGACTGATTAAGATGCTGATGATGATGATGATGATGATGATGATG 974
Db 901 GAGGATCTAGGACTGATTAAGATGCTGATGATGATGATGATGATGATGATGATG 960
OY 975 ATTACAGTTATTAAGATGACACAGTAAATGTTGAGAGTTTCAAGAGTATTT 1034
Db 961 GTGACCGTGGACAAAGATGACAGGTTATTTGAGAGTTTCAAGAGTATTT 1020
OY 1035 GCTAACCGTATTCAGTATTAATGCAATTTAGAAACAACTTGCAGTTTGAACGT 1094
Db 1021 TCTCAGCGTGTGCTGATTAAGTCTCAATGCAATGCAATGCTTGAATTTGACCGT 1080
OY 1095 GAAAAAATCAAGAGTGTGCGAAATTAAGTGTGCTGATGATTAAGAGTATTA 1154
Db 1081 GAAAAAATCAAGAGTGTGCGAAATTAAGTGTGCTGATGATTAAGAGTATTA 1140
OY 1155 GCTCAACAGACAGCTTTAAAGAAATGCAATGCAATGAGGATGCTTAATGCT 1214
Db 1141 GCTCAACAGCTTTAAAGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCT 1200
OY 1215 ACAGTGCAGCGCTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1274
Db 1201 ACTGCTGACAGCTTTGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
OY 1275 ATTGAAAAAGTACAGCTCTTGAAGCTTGAAGAGTATGCTGCTGCTGCTGCTGCT 1334

```

```

Db 1261 ATTCACGCTGTGCTACTGGAATTGACAGAGATGACCAACAGAGCTAATTTGTT 1320
OY 1335 CTTCGCTCTTAAGAACGCTGTAGCTCAATTTGCTTAATGCTGGTACAGAGCTTC 1394
Db 1321 CTTCGCTCTTGAAGAACGCTGTGCTCAATTTGCTCAATGCTAGAGATTTAGAGATCT 1380
OY 1395 GTAGTTATGACAAAGTTGAAAAACAGCCCTGACAGAACAGAGATTTAATGCTGACAGAGT 1454
Db 1381 ATGCTATTCATGCTTTGAAAAATGCTGAGCTGTGATGATTAACAGACAGAGCTGAC 1440
OY 1455 GAGTGGTATATGATTAAGAACAGATTCATTAACCTGTCAAATGACAGATCAGC 1514
Db 1441 GAGTGGTATTAAGTATGATCAAGATTCATTAACCTGTCAAATGATGATGCTGTCACCC 1500
OY 1515 CTTCAAATGCACTCTGCTAGCTGATGCTTATTTTGAACAGACAGAGCTTGTGCTAAT 1574
Db 1501 CTACAAATGCACTCTGCTAGCTGATGCTTATTTTGAACAGACAGAGCTTGTGCTAAT 1560
OY 1575 AACCCTGACAGCTACCGCAGCCGACAGCATGCGACAGATGATGATCAGAGATGATG 1634
Db 1561 AACCCTGACAGCTACCGCAGCCGACAGCATGCGACAGATGATGATGATGATGATG 1620
OY 1635 GGATG 1638
Db 1621 GGAG 1624

RESULT 6
AF117741 2401 bp DNA BCT 06-APR-1999
LOCUS AF117741
DEFINITION Streptococcus pneumoniae strain CP1200 co-chaperonin GroES (groES)
and Chaperonin GroEL (groEL) genes, complete cds.
ACCESSION AF117741
VERSION AF117741.1 GI:4566771
KEYWORDS
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 2401)
AUTHORS Kim,S.N., Lee,J.Y., Kim,S.W., Choi,I.H. and Rhee,D.K.
TITLE groESL sequences in Streptococcus pneumoniae
JOURNAL Unpublished
PUBMED 2 (bases 1 to 2401)
AUTHORS Kim,S.N., Kim,S.W., Choi,I.H. and Rhee,D.K.
JOURNAL Direct Submission
SUBMITTER Submitted (04-JAN-1999) Pharmacy, Sungkyunkwan University, 300
Chunchun-dong, Suwon, Kyunggi-Do 440-746, Korea
FEATURES
source
1..2401
/organism="Streptococcus pneumoniae"
/strain="CP1200"
/db_xref="taxon:1313"
122..603
/gene="groES"
122..127
/gene="groES"
147..152
/gene="groES"
262..288
/feature="controlling inverted repeat of chaperonin
expression"
1..2401
/feature="CIRCE"
1..311
/feature="inverted
RBS 307..311
/gene="groES"
319..603
/gene="groES"
/codon_start=1
/transl_table=11
/product="co-chaperonin GroES"
/protein_id="ABD23454.1"
/db_xref="GI:4566772"

```



```

/translation="MKRPLGDRVLKIEKEQTVGSGFVLASQEKTKTAQVAATGCG
VRLKGDLYAVSVKTDGRLVEAHAGLDVKGDEKTIIVGENMILAIIEE"
606..2241
/gene="groEL"
RBS 606..610
/gene="groEL"
CDS 619..2241
/gene="groEL"
/codon_start=1
/transl_table=11
/product="Chaperonin GroEL"
/db_xref="GI:456773"
/translation="MSKEIKFSSDARSAMVRCVDLADTVKVTGLPKDRNVLEKSPG
SPLINDGVITAKEIELEDHFNENKAKIVSEIASKNDIADGGTTATVLOAVRG
IKNTVAGANPIGIRRGIEIAVAAVEALKNNAIIPVANKSEIISOVAVSSREKVEYI
SEAMEKVGKDVITIEESRGMELEEVGMOFDGXYISQVWYDSEKMAVDLENPIYI
LITDKKISNIOEILPLESILIOSNRPILLIADUGSEALPTVYLNKIRGTFNVYAKA
RPGGRKRAMLEDIAITIGSTVTTEDLGLKDATIEALGMAKRYTDKSDYVBA
GNPEAISHRAVIVKSQIEITTSERDEKIQERLAKLSGVAVIKVGAATTELKMKL
RIEDLNATRAVEGIVAGGTALANVIPAERTIELGDEDTGNIVLRALBEPVRO
IAHNAGFEKSLVIDRLKNAELIGFNAAGVNMIDGIIIDPVKVSRLAONASVA
SLITTEVAVNKPPEVAPAPAMPDMGMGM"
2274..2302
terminator 743 a 459 c 568 g 631 t
BASE COUNT
ORIGIN

Query Match 62.0%; Score 1030.6; DB 1; Length 2401;
Best Local Similarity 77.2%; Pred. No. 9.2e-197;
Matches 1252; Conservative 0; Mismatches 369; Indels 0; Gaps 0;

14 TATGGCAAAAGAAATCAATTTTCAGCAGATGCGGTGTCATGTCGCGGAGATTGA 73
Db 618 TATGTCAAAAGAAATTAATTTTCATGATGATGCCGTTCAGCATGTCGTGCTGCA 677

74 TATGTACGAGATACCGTCAAGTAAAGCTGTCTTAAAGGCGCATATGTTCTTGA 133
Db 678 TATCTTGGCAACAGCTTTAAAGTAACTTGGGACCAAAAGATCGCAATGTCTTGA 737

134 AAAAGCTTTGGTTCCTTAACTAATGAGCGGTAACCATTCCTAAGAGATGCA 193
Db 738 AAAAGTATTCGTTACCTGATACCAATGAGGATGACCATTCGCCAAAGAAATGA 797

194 ATTAGAAGATCAATTTGAAACATGCGGCAAAATGCTGTGAAGTGGCTTCAAAAC 253
Db 798 ATTGGAAGACATTTTGAATAATGGGTGCTAAGTTGATCGAATAATGCTTCAAAAC 857

254 CAATGATATTGCTGTGATGAGCAGACTACTGCAACAGTTTTCACACAGCCATTGTTCA 313
Db 858 CAATGATATCGGAGGTGACGGAGTACGACACTGCAACAGTCTGACCAAGATATGTCGG 917

314 TGAAGACTAAAAAATGAGCAGCGAGTGTCAATCAATGGATCCGTCGAGCATTTGA 373
Db 918 TGAAGGATCAAAAAACGTACACAGAGTGGCAATTCATTCGATTCGTGAGGATTTGA 977

374 AACACGACACGACAGCTGTTGAAGCCTTGAAGCCATGCTCAACCTGTATCTGGCAA 433
Db 978 AACAGCAGTTCGCGCAGAGTTTGAAGCCTTGAAGAAACAGCCATCCCTGTGCAATAAA 1037

434 GGAAGCTATTGCTCAGTGTGCTGACATCATCAGCTGTGAAGAAAGTTGGAGATATAT 493
Db 1038 AGAAGCTATCTCAAGTTGAGCGCATCTCTCTGTTGAAAAAGTTGGTGAATCAT 1097

494 CTGAGAAGCTATGAGCTGTGGCAACGATGCTGATTTACATCGAAGATCTCGAG 553
Db 1098 CTCTGAAGCAATGAAAAAGTTGGCAAAAGCGGTGTCACCATCGAAGATCACGGTG 1157

554 TATGAAACAGAACTTGAAGTGTGAAGCATGCAATTGACCGGTGTTACCTGTCA 613
Db 1158 TATGGAACAGAGCTTGAAGTGTGAAGGATGCAAGTTGACCGGTGTTACCTTTGCA 1217

614 ATACATGCTCAGACATGAAAAAATGTTGCAAGACTTTGAAAAACCATTTATCTTAAT 673

```

```

||||| 1218 GTACATGCTACGATGAGAGCAAAAAATGCTGGCTGACCTGAAAAATCCGTCATTTGAT 1277
Oy 614 CACGATAAAAAAGTGTCAAAACATCCAGACATTTTCCACCTACTGAGAGAGATCTTAA 733
Db 1278 TACAGACAAAAAATTTCCATATTCAGAAATTTTCCACTTTTGGAAAGCATTTGCA 1337

734 AACCAACCGTCCATTAATCTATTATGACATGATGATGATGATGTAAGACACTTCCAACT 793
Db 1338 AAGCAATCGTCCACTTCTATTATGCGAGATGATGATGATGATGATGATGATGATGATG 1397

794 TGCTTGAACAAGATTCGTGACTTTCATGATGATGATGATGATGATGATGATGATGATGAT 853
Db 1398 TGTTTGAACAAGATTCGTGACTTTCATGATGATGATGATGATGATGATGATGATGATGAT 1457

854 TGATCGCTGTAAGCTATGCTTGAAGACATTTGATGATGATGATGATGATGATGATGATGAT 913
Db 1458 TGACCGCTGTAAGCTATGCTTGAAGACATTTGATGATGATGATGATGATGATGATGATGAT 1517

914 AGAGATCTAGACCTTGAATTAAGATGCTTAACATGACAGCCCTTGACAGGCTGTAA 973
Db 1518 AGAAGACCTTGTGCTTGAATTAAGATGCTTAACATGACAGCCCTTGATGATGATGATG 1577

974 GATTACGTTGAATAAGATGACACATTAATTTGTAAGCTTGCAGAACTTGCAGAACTAT 1033
Db 1578 AGTACCGTGAATAAGATGACACATTAATTTGTAAGCTTGCAGAACTTGCAGAACTAT 1637

1034 TGCTAACGTTATGCTGATTAATATGCAATTAAGAAACACAACTTGTGATTTGACCG 1093
Db 1638 TTTCACCGGTTGCTGATTAATATGCAATTAAGAAACACAACTTGTGATTTGACCG 1697

1094 TGAATACTAAGAAAGCTTTGGGAAATAGCTGCTGATGATGATGATGATGATGATGATGAT 1153
Db 1698 TGAATACTAAGAAAGCTTTGGGAAATAGCTGCTGATGATGATGATGATGATGATGATGAT 1757

1154 AGCTCCAGAGAGACGCTTTAAAGAAATGAAATTCGATGATGATGATGATGATGATGATGAT 1213
Db 1758 AGCGCGACGCTGAAAGCTTTGAAAGAAATGAAATTCGATGATGATGATGATGATGATGAT 1817

1214 TACAGTCAGCGCTTGAAGAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1273
Db 1818 TACTCGTCAGCTGTTGAAGAAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1877

1274 TATTGAAAAAGTACGACTTTGAGCTTGAAGGCTGATGCTACTGACGTAACATTTG 1333
Db 1878 GATTCCAGCTGAAAGCTTTGAGCTTGAAGGCTGATGCTACTGACGTAACATTTG 1937

1334 GCTTCGCTGCTAGAAAGCTGTAACGCTCAATTTGCTTAAATGCTGCTGCTGCTGCTGCTG 1393
Db 1938 TCTCGCTGCTTGAAGAAAGCTGTAACGCTCAATTTGCTTAAATGCTGCTGCTGCTGCTG 1997

1394 CGTATGTTGCAAGTTGAAAAACGCTTGCAGAACAGATTTAAATGCTGCAACAG 1453
Db 1998 TATCGTTATGATGCTTTGAAAAATGCTGAGCTTGTATGATGATTTAAACGAGCAACTG 2057

1454 TGAAGTGTGATGATTAACAGCAATCATTTGACCTGTCAAAAGTAAACAGATCAGC 1513
Db 2058 CGAGTGGTTAATCATGATGATTAACAGCAATCATTTGACCTGTCAAAAGTAAACAGAT 2117

1514 GCTTCAAAATGCAAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1573
Db 2118 CTTCAAAATGCAAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2177

1574 TAAACCTGAAACAGCTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1633
Db 2178 TAAACCTGAAACAGCTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2237

1634 G 1634
Db 2238 G 2238

```

RESULT 7

AE006276 12560 bp DNA BCT 09-FEB-2001  
DEFINITION Lactococcus lactis subsp. lactis IL1403 section 38 of 218 of the complete genome.  
ACCESSION AE006276 AE005176  
VERSION AE006276.1 GI:12723260  
KEYWORDS  
SOURCE Lactococcus lactis subsp. lactis.  
ORGANISM Lactococcus lactis subsp. lactis  
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Lactococcus.  
REFERENCE 1 (bases 1 to 12560)  
AUTHORS Bolotin,A., Mincker,P., Mauger,S., Jallion,O., Malarme,K., Weissenbach,J., Ehrlich,S.D. and Sorokin,A.  
TITLE The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
JOURNAL Genome Res. (2001) In press  
REFERENCE 2 (bases 1 to 12560)  
AUTHORS Bolotin,A., Mincker,P., Mauger,S., Jallion,O., Malarme,K., Weissenbach,J., Ehrlich,S.D. and Sorokin,A.  
TITLE Direct Submission  
JOURNAL Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France  
FEATURES  
source  
1..12560  
/organism="Lactococcus lactis subsp. lactis"  
/strain="IL1403"  
/sub\_species="lactis"  
/db\_xref="taxon:1360"  
129..320  
/gene="yjdB"  
/note="L195067"  
129..320  
/gene="yjdB"  
/note="EVIDENCE BY GENEMARK BIO16.01 UNKNOWN. General. homologs not detected in Streptococci."  
/codon\_start=1  
/transl\_table=11  
/product="UNKNOWN PROTEIN"  
/protein\_id="AAK04486.1"  
/db\_xref="GI:12723261"  
/translation="MIHETDRAOHSTKIDAFWIEPPTGALFEGGLVSEKNAI  
TFEINKTLEVEFEKNEKIT"  
362..679  
/gene="trxB"  
/note="L195348"  
362..679  
/gene="trxB"  
/note="EVIDENCE BY HOMOLOGY BIO02.10 Thioredoxin, glutaredoxin, and glutathione. similar to the thioredoxin H-type from plants."  
/codon\_start=1  
/transl\_table=11  
/product="thioredoxin H-type"  
/protein\_id="AAK04487.1"  
/db\_xref="GI:12723262"  
/translation="MIPEENIENLAEDVKGPEKTFEFTAGCGDCNFKPKRETEY  
ENPDFEVEVDDEMDLAIDEMGIMPSPVIEDGKEKARLVNKKRTEEVNTLA  
SAR"  
765..1391  
/gene="yjdD"  
/note="L195751"  
765..1391  
/gene="yjdD"  
/note="EVIDENCE BY HOMOLOGY BIO15.01 HYPOTHETICAL. homolog to YPR\_B subtilis, has local similarity to similarity to phenylalanine tRNA ligase"  
/codon\_start=1  
/transl\_table=11  
/product="HYPOTHETICAL PROTEIN"  
/protein\_id="AAK04488.1"  
/db\_xref="GI:12723263"  
/translation="MIATYNTNVGDVIMLTITANDKGEKVFERRKGVAVFIETGAT

gene  
1354..2894  
/gene="noxE"  
/note="L196579"  
1554..2894  
/gene="noxE"  
/note="EVIDENCE BY HOMOLOGY BIO06.01 ENERGY METABOLISM. aerobic."  
/codon\_start=1  
/transl\_table=11  
/product="NADH oxidase"  
/protein\_id="AAK04489.1"  
/db\_xref="GI:12723264"  
/translation="MKIVIGTINMAGIATANTLIDRYGHEIYIMDRSNMNYLGGCT  
AIVGROIEKPEDELYAKAEDEFEKKYKILTEFESEIDFNKMYIAKSTGKRTES  
YKLVATGSRPITPNLPGDINGIHFKILPFGGALIDEPKADYKRIAVIAGITG  
TEIARAKRRCREVLIDPAESTLASIYDEBRAGKMDENLAHIGELAFGLQETRA  
NKGVSQIVYINKSTYDVLINCIGITNASKVLASGHELETRKNAIVDRHQSSQDP  
VSAVDVATITSNALODPTIYALASNAVSGIVAGHNIGSGIESVGVQSGNSISIG  
YMTSTGLSVAAKIGLEVSFSDFDKQKAMFLHENDSVKIRIIVETNRRIIGAO  
LASKSEIIAGNINMSELAIOEKRTIDELALDLFLPHFNSPYMTVAALNNAK"  
2984..3373  
/gene="sbaA"  
/note="L0299"  
2984..3373  
/gene="sbaA"  
/note="EVIDENCE BY HOMOLOGY BIO10.02 DNA replication, restriction, modification, recombination, and repair. THIS PROTEIN IS INVOLVED IN DNA RECOMBINATION AND REPAIR"  
/codon\_start=1  
/transl\_table=11  
/product="single-strand binding protein"  
/protein\_id="AAK04490.1"  
/db\_xref="GI:12723265"  
/translation="MNTKMLIGRLTSAPISRTNDKSYVAVTIANRRKRNKERE  
ADFSIIIMWSAETIYVSKKSLISIGELIRNTYIDKONAHYTELIGSLDIL  
BSRATIARESAITEETLDAELPF"  
3493..3777  
/gene="groES"  
/note="L198515"  
3493..3777  
/gene="groES"  
/note="EVIDENCE EXPERIMENTAL PMID:8486277 BIO04.03 Chaperones"  
/codon\_start=1  
/transl\_table=11  
/product="10 KD chaperonin"  
/protein\_id="AAK04491.1"  
/db\_xref="GI:12723266"  
/translation="MLKPLENRVYLVKKEEKSNGGIVLTSAOSEKPOTAEVAVNGE  
GKTNNHGTLSPLVKGDTVIFEFKAGTIVAKMDEEFLIKDSDLAIEY"  
3865..5493  
/gene="groEL"  
/note="L198893"  
3865..5493  
/gene="groEL"  
/note="EVIDENCE EXPERIMENTAL PMID:8486277 BIO04.03 Chaperones"  
/codon\_start=1  
/transl\_table=11  
/product="60 KD chaperonin"  
/protein\_id="AAK04492.1"  
/db\_xref="GI:12723267"  
/translation="MSKDIKFSDDARTAMRGDIIADIVKTTGLGKGRNVLEKSYG  
SPLITNGVITAKEIELEDHEDFNMGAKVSEVASKTINDIGDGTATVATLVAIYREG  
LKNYTAGANVGIIRGIEIAETAVASIKEMAIIVHDKSAIAQVAVSSSEKVEYI  
SDAMERVGSDGVITIEESKQTELDVVEGQDFRGYLSQYVSNTERKVAELDPYI  
LIDPKKISNIOELIPLLEOILKTRNPLIIVADVGGALPTLVNKKIKGVFNVAVKA  
PGFDRRAKOLEDLATITGGVITVEIGLIDKDTALEALGOAAKATVDQDHTIYEGA  
GSDAISDRVAITIKAOIETKTSDDPRELORLAKIAGVAVYKGAATETELAMKL  
LIDBALNAPRAVBERIVSGGTALVNAIALDLKSEBDIGTGINIYARALEEPRQ



```

Db 5121 TCGATTGCTGCTTGGATTAACCTTTCAGAGAGAGATATTCACAGCTATTAACAT 5180
Qy 1331 TGTGCTTCCTGCTCTAGAGAGAGCTGTACCTCAAAATGCTTAATGCTGGGTACGAGG 1390
Db 5181 TGTTCGCGCTGCTCTTGAAGACAGCTTCTCAAAATGCTGTGCAATGAGATATGAGG 5240
Qy 1391 CTCGAGTATTGACAGTGAAGAACCCCTGAGAGACAGATTTATGCTGCAC 1450
Db 5241 TTCAGTTATCATTTGATTAACCTGCTTACAGAGAGATGATGACGATTCATGCTGCAC 5300
Qy 1451 AGGTGAGTGGTGTATGATTAACAGAGATCATTTGACCTGTCAAGTAACAGATC 1510
Db 5301 TGTGATATGGGTTATATGATTAAGAGAGATGATGACCTGCAGAAAGTAACCTGCTC 5360
Qy 1511 AGCGCTTCAAAATGACAGCTCTGTAGTATGCTTATTTGACACAGAGAGCTGTGCG 1570
Db 5361 AGCTTTCAGAAACGGGGTCTGTGTGCTTTATTTGACTACTGACAGAGATGATGCTC 5420
Qy 1571 TATAAACCCTGACACCTACGACGAC 1597
Db 5421 TATTAAGCCAGACCGCTGCTCCAGC 5447

RESULT 8
LOCUS LGROESEL 2267 bp DNA BCT 12-MAR-1993
DEFINITION L.lactis groes and groEL genes.
ACCESSION X71132
VERSION X71132.1 GI:287869
KEYWORDS groEL gene; groes gene; heat shock protein.
SOURCE Lactococcus lactis.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
REFERENCE 1 (bases 1 to 2267)
AUTHORS Kim, S.G. and Batt, C.A.
TITLE Cloning and sequencing of the Lactococcus lactis subsp. lactis. .
JOURNAL Gene In press
AUTHORS 2 (bases 1 to 2267)
Batt, C.A.
DIRECT SUBMISSION
SUBMITTED (04-MAR-1993) C.A. Batt, Cornell University, 107 Stocking
Hall, Ithaca, NY 14853, USA
FEATURES
source
1. 2267
/organism="Lactococcus lactis"
/strain="ssp. lactis"
/isolate="CC9"
/db_xref="taxon:1358"
194..220
/note="heat shock motif"
246..530
/gene="groes"
246..530
/gene="groEL"
/codon_start=1
/transl_table=1
/protein_id="CAA50445.1"
/db_xref="GI:287870"
/transl_table="MLKPLENRVLRVKEEEKSMGIVLTSASOKPOTAEVAVGE
GKTNHGILISPLVKVGVIVIFEKFRAGTVKAKDEFLIKDSDLAIVE"
618..2246
/gene="groEL"
618..2246
/gene="groEL"
/codon_start=1
/transl_table=1
/protein_id="CAA50446.1"
/db_xref="GI:287871"
/transl_table="MSKDKFESSDARTMMAGIDILADIVKTTLGGKGRNVLEKSYG
SPLITINGVTIAKEIELEVEHFNMGAKLVSEVASKTNDIAGDGTNTATVLTQALVREG

```

```

Query Match 57.1% Score 948.6; DB 3; Length 2267;
Best Local Similarity 74.9%; Pred. No. 2,5e-180;
Matches 1188; Conservative 0; Mismatches 399; Indels 0; Gaps 0;

BASE COUNT 763 a 357 c 487 g 660 t
ORIGIN
LKNVTAGNPGVIRGICELAEFAVAIREKMAIPVHDKALIAQVATVSSREKVEYI
SDAMERVGSDVITITIEESKQJLELDVBEQMDKRYLSQVWSTEMKVELNDPII
LITDKRISNIOELPLLEJLITKILTRPPLIYADVDDEALPTLVKRIQVNVAVNA
PQGDHRRKQLEHLALINGVLTITIEELGDLKMLATEALGAQAKTKVKBHETIVEGA
GSADAIISDRVAIKQIKRITSDREKLOERAKLAGVAVKVGATFETLEKML
LEEDALNTAAVVEGIVSGGATLVAALDLKLEESDIDGTGINTIYRALLEPVO
IANNAGFBSVYIDKLRSEEGTFNNAATGOMVNTIEESIVDPKAVTRSAIONNASVA
GLITTEAVANKPEPPAPAMPDPDPSMGSMI"

Qy 11 TCATATGCAAAAGAAATCAAAATTTTCAGCAGATGCGGCGTGCCTGCTGGGGAGT 70
Db 614 TAAATGTCAAAAGATATTAATTTTCAAGTATGCTAGACAGCATATGCTGGAGT 673
Qy 71 TGATATGTAGCATACCGTCAAGTAACCGTTGTCCTTAAAGGCGCAATGTTGCT 130
Db 674 TGATATCTGTGATACAGTAAACACACCTTGACCAAAAGTGCAGATGTTGCT 733
Qy 131 TGAAGAAGCTTTTGTTCCTTAACTATAGAGGGGTAAACCATTTGTAAGAGAT 190
Db 734 TGAAGAAATCATATGATCATCTTTAATTAACAAGATGATGTAACATTTGCCAAGAGAT 793
Qy 191 CGAATTAGAGATCATTTTGAAGAACATGGAGCAAAATTTGCTCGAAGTGGCTTAA 250
Db 794 TGAACCTTGATACATTTTGAAGAAATGAGGCTTAACTTGTTCGAAAGTTGCTTCAA 853
Qy 251 AACCAATGATTTGCTGTGATGAGGACACTACTGCAACAGTTTGTGACACAGCATTTGT 310
Db 854 AACCAATGATTTGCGAGGAGGAGGACGACAAACACAGCAGATTTGTGACACAGCATTTGT 913
Qy 311 TCATGAGAGACTAAAAATGTGACAGAGGCTGCAATGCAATGTGATCCGTCCAGCAT 370
Db 914 TCGTGAAGGTTTAAAAAATGTTTACCGAGTGCAATCGTTGATTCGCGAGGAGAT 973
Qy 371 TGAACACGACACACACAGCTGTGAAGCTTGAAGCCATTTGCTCAACCTGATATCG 430
Db 974 TGAACCTTGTGTGAAGACGCTGTGCTCAATTAAGAGATGAGCAATTCCTGTCACGA 1033
Qy 431 CAAGAGAGCTATTTGCTGAGTGCCTGATATCATACCTGCAAGAAAGTTGAGAGTA 490
Db 1034 TAAATCAGCAATTTGCGCAAGTACCTGTTATCATCAGTATGAAAAGTGGTGAGTA 1093
Qy 491 TATCTAGAGAGTATGAGGCTGTGGCAACGATGTTGATTAACATGAAAGATCG 550
Db 1094 TATTTCTGATGCAATGAGACGTTGTTGTAAGGAATGCAATTTGACCTGGATTTTGAG 1153
Qy 551 AGGTATGGAACAGAACTTGAAGTGTGAAGGATGCAATTTGACCGTGTACCTGTC 610
Db 1154 AGGATGCAAACTGAACTGATGTTGTTGAAGGAATGCAATTTGACCTGGATTTTGAG 1213
Qy 611 TCAATATATGTCACAGCAATGAAAAATGTTGACACTTGAANAACCATTAATCTT 670
Db 1214 TCAATATATGTTCTATATACAGAAAAATGTTGTAATTAATCTTATTTCT 1273
Qy 671 AATCAGGATTAAGAAATGTCAAACATCCAGACATTTGCACACTTGAAGAGTTCT 730
Db 1274 TATTAACGACAAAAAATCTCAAAACATTCAGAAATTTTACCGCTCTGACAAATCTT 1333
Qy 731 TAAACCAAGCTGCTACTTATATGCAATGATGATGATGATGATGATGATGATGATGAT 790
Db 1334 GAAAAACAATGCTCACCTCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1393
Qy 791 CTTGCTTGAACAAGATGCTGATCTTCAATGATGATGATGATGATGATGATGATGATGAT 850
Db 1394 GCTTCTTCTTAATTAAGATTAAGTGTCTTCAATGATGATGATGATGATGATGATGATGAT 1453
Qy 851 TGTGATGCTGTGAAGCTATGCTTGAAGACATGCTATCTTGAAGAGTGTACAGTAT 910

```

```

Db 1454 TGGTGATCGTGTAAAGCTCAATTGGAACATTTGCGTCTCTGACAGCTGTACATAT 1513
Qy 911 TACAGAGATCTAGAGCTTGAATTAAGAGTCTCAATGACACCCCTTGACAGCTGC 970
Db 1514 TACGGAAGACCTGGCTGATCTTAAGATCTCTTAAACCTTTAGACACAGCAGC 1573
Qy 9/1 TAAATTAACAGTTGAATAAAGATAGCAGATATTTGTAAGAGTTCAGAGAGTTCAGAGC 1030
Db 1574 TAAAGCAACGTGGATTAAGACACCAACATTTGTAAGAGTCTCTCTCTCATGC 1633
Qy 1031 TATTGCTACCGATTTGCTACATTAATCGCAATTAAGAAACAACCTTCTGACTTGA 1090
Db 1634 TATTGCTACCGATTTGCTACATTAATCGCAATTAAGAAACAACCTTCTGACTTGA 1693
Qy 1091 CCGTGAACAACTACAAAGAGCTTTGGCGAAATTAAGCTGTGTAGCTGTATCAAGT 1150
Db 1694 TCGTGAACAACTACAAAGAGCTTTGGCGAAATTAAGCTGTGTAGCTGTATCAAGT 1753
Qy 1151 AGGAGCTCCACAGACAGCCTTTAAAGAAATGAACCTTGCAATGAGAGCTCTTAA 1210
Db 1754 TGGTGTGCTGCAACTGAACAGAGCTCAAAAGCAATGAACCTTGCAATGAGAGCTCTTAA 1813
Qy 1211 TGTCAACAGCTGCAAGCCCTTGAAGAGATATGCTGTGCTGTGAGAGCACTATATAC 1270
Db 1814 TGAACACAGCTGCAAGCCCTTGAAGAGATATGCTGTGCTGTGAGAGCACTATATAC 1873
Qy 1271 GGTATTTGAAAAAGTGAAGCCTTTGAGCTTGAGAGGCGAGATGCTACTGAGAGTAACT 1330
Db 1874 TGTATTTGAGCTGCTTTGATTAACCTTTGAGAGAGAGATTTCAAAAGATTAACAT 1933
Qy 1331 TGTGCTGTGCTGTCTAGAAAGAGCTGTACGCTCAATTCCTTTAATGCTGTGAGAG 1390
Db 1934 TGTGCTGTGCTGTCTAGAAAGAGCTGTACGCTCAATTCCTTTAATGCTGTGAGAG 1993
Qy 1391 CTCGCTGATTAATGAACAGCTGTAACAAAGCCCTGCAAGAAAGATTAATGCTGTGAG 1450
Db 1994 TTTCAATTAATGATTAATGAACAGCTGTAACAAAGCCCTGCAAGAAAGATTAATGCTGTGAG 2053
Qy 1451 AGGTGACTGGCTGATGATGATTAATAACAGAAATCATGACCTGTCTCAAGTAAACAGATC 1510
Db 2054 TGGTCAATGGCTGATGATGATTAATAACAGAAATCATGACCTGTCTCAAGTAAACAGATC 2113
Qy 1511 AGCCCTCAAAATGAGCTTCTGTAGCTAGCTATATTGTAACAAAGAGAGAGTGTGTC 1570
Db 2114 AGCTTGTCAAAAGAGCGGCTTCTGTGCTGTGCTGATTAATTTGACTACTGAAACAGTACTTGC 2173
Qy 1571 TAAATTAACCTGAACAGCTAGCCGACG 1597
Db 2174 TAAATTAACCTGAACAGCTAGCCGACG 2200

RESULT 9
LOCUS AY029215 2187 bp DNA BCF 16-Apr-2001
DEFINITION Lactococcus lactis subsp. cremoris chapetonin Groes and chapetonin
ACCESSION AY029215
VERSION AY029215.1 GI:13641349
SOURCE Lactococcus lactis subsp. cremoris.
ORGANISM Lactococcus lactis subsp. cremoris.
REFERENCE 1. (bases 1 to 2187)
AUTHORS Vogensen, F.K. and Kilstrup, M.
TITLE groELs sequence from Lactococcus lactis subsp. cremoris MG1363
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 2187)
AUTHORS Vogensen, F.K. and Kilstrup, M.
TITLE Direct Submission
JOURNAL Submitted (04-Apr-2001) Department of Dairy and Food Science, The
Royal Veterinary and Agricultural University, Rolighedsvej 30,

```

```

FEATURES             Frederickberg C 1958, Denmark
                     Location/Qualifiers
                     source
                     1. 2187
                        /organism="Lactococcus lactis subsp. cremoris"
                        /strain="MG1363"
                        /sub_species="cremoris"
                        /db_xref="taxon:1359"
                        complement(44..60)
                        /note="putative"
                        /bound_molecule="Cler"
                        83..109
                        /note="CIRCE element; putative"
                        84..89
                        /note="putative"
                        107..112
                        /note="putative"
                        121..125
                        /note="putative"
                        134..418
                        /note="Cpn10-11ke"
                        /codon_start=1
                        /transl_table=1
                        /product="Chapetonin Groes"
                        /protein_id="AAK11638.1"
                        /db_xref="GI:13641350"
                        /translation="MKPLRNRYVLRVREKESKMGIVLTSASQKPTQAEIVANG
                        GRTNHGTLISPLVKGVDIVFEKFAITVKNMGDEFLIKDSLLAIYE"
                        425..452
                        496..499
                        /note="putative"
                        505..2133
                        /note="Cpn60-11ke"
                        /codon_start=1
                        /transl_table=1
                        /product="Chapetonin GroEL"
                        /protein_id="AAK11639.1"
                        /db_xref="GI:13641351"
                        /translation="MSKEIFSSDARTAMRCIDLDVYKTTLGPGRNVLEKSYG
                        SPLINDSVITAKIELEDEHFEENMGAKLVEVASTKNDIADGTTATVYLTQAIYREG
                        LKNTVAGSNPVGIRGIELAEYAVASIKEMAIPIVHDKSAIQAIVASVSRSEVEYI
                        SPAMERVASNDVITIEESKMGOMELDVVEGQFQDGYLSQVMSNTEKMAVEIDNPYI
                        LITDKKINIDELIPLDQILKTRNPLIIVADVDGEXALPTLVNKKIKGVFNVAVKA
                        PEGGRKRAQLEDLALITGGTVTEELGLDKDNLTELGQAKAVYDQHTTIVEGA
                        GSEVASISRVAVIIRAOIETKTSDFOREKLOERLKLGGVAVYVGAARETELKAMKI
                        LIEADLNTPRAVVEGIVSGCGATLYNATAALDKLSEGDIOGICINVRALPEPVRQ
                        IAAANGTGSYIIDKLSEKVGTRMAATGVNANIEGIVDPKVTYRSLQVAAVSA
                        GLITTEAVVANKPEPAAPAMPMDPSMGGM"
                        2139..2162
                        /note="putative"
BASE COUNT 735 a 353 c 474 g 625 t
ORIGIN
Query Match 56.7%. Score 942.2; DB 2; Length 2187;
Best Local Similarity 74.6%; Pred. No. 4.8e-179;
Matches 1184; Conservative 0; Mismatches 403; Indels 0; Gaps 0;
Qy 11 TCATATGGCAAGAAATCAATTTTACAGAGATGCGCGTGTGCCATGTGCGCGAGT 70
Db 501 TAAATGTCTAAAGAAATTAATTTTCAAGATGCTAGAACAGAGATGCGCGGAAT 560
Qy 71 TGAATGTGAGAGATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 130
Db 561 TGAATTTCTTCCCGATACAGTAACCAACCTTTGGCCCAAAAGGCGTAATGTTTCT 620
Qy 131 TGAAGAGCTTTGGTCTCCCTTAATTAATGAACGGGGTAAACCATGCTTAAAGAT 190
Db 621 TGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
Qy 191 CGAATTAAGAGATCAATTTGAAGAAATGAGGAGCAAAATGAGTGTGAAGTGTCTAA 250
Db 681 TGAATTTGAAGACCATTTTGAAGAAATGAGGAGCAAAATGAGTGTGTGGAAGTGTCTAA 740

```

```

OY 251 ACCAATGATTTGCTGGTGGATGGAGACTACTGCACAGTTTGGACAAAGCATTTG 310
DB 741 AACAAATGATTTGCGAGGTGATGGACACACAGGACAGTTTGGACAAAGTATTTG 800
OY 311 TCATGAGAGACTAAAAATGTGACAGAGGTGCTATCCAAATGGTATCCGTGAGCAT 370
DB 801 TCGTGAAGATTTGAAAAATGTTACTGACAGGTGCAAAATCCAGTGTATTCGCCAGAA 860
OY 371 TGAACACGACACAGACAGCTGTTGAAAGCTTGAAGCCATTGCTCAACCTGTATCTG 430
DB 861 TGAATCGGACGTGAACAGACAGTTCCTCAATTAAGAAATGCAATTCCTGTTACGA 920
OY 431 CAAGAGCTATTGCTGAGTCTGCTGACATATCATACCCCTGAAAAAGTTGGAGATG 490
DB 921 TAAATACGCAATCGCTCAAGTTGCTACCGTTTATACGTAGTGAAGAAAGTTGGGAAT 980
OY 491 TATTCAGAAAGTATGAGAGCTGTGGGCAACGATGTGTGATTAACATCGAAGATCTG 550
DB 981 TATTTCTGACGCAATGGAGCGCTGTAAGTTCTGACGAGTATCAAAATCGAAGATCAA 1040
OY 551 AGGTATGGAACAGAACTTGAAGTGTGAAGCATGCAATTTGACGCTGATACCTGTC 610
DB 1041 AGGAATGCAAAACAGAGCTGATGTTGTGAAGAAATGCAATTTGACCGTGTGATGAG 1100
OY 611 TCATATCATGTCACACAGCATGAAAAATGTTGCAAGCTTGAAACCATTTATCTT 670
DB 1101 TCATATATGTTTCTAATACAGAAATGTTGCTGATGATATATCTTATATCTT 1160
OY 671 AATCAGGATTAATAAAGTGTCAAAATCCAAACATTTGCGACTTACTGATGAGAACTCT 730
DB 1161 GATACGGAATAAAAAATCTCAAAATTCAGAAATTTTACCGTTTTCAGAAATTTT 1220
OY 731 TAAACCAACGCTCATCTACTCATATATGCAATATATGATGATGATGATGATGATGAT 790
DB 1221 GAAAAAATGCTCCACTTTTAATTTGCTGATATATGATGATGATGATGATGATGATG 1280
OY 791 CCTGTCTTGAACAAGATTCGTGATCTTCAATGTTGCTGCTCAAGCCGACGAT 850
DB 1281 TCTTGTCTTAAATGAATTAAGGCTTCAACCTGATGCTGATTAACACCGGAT 1340
OY 851 TGGTATGCTGTAAGCTATGCTTGAAGACATTCCTGCTGACAGGTGATGATGATGAT 910
DB 1341 TGGTACCGCGTAAAGCTCAATGTAAGATTTAGCTTCTGACAGGTGATGATGATGAT 1400
OY 911 TACAGAGATTAAGATTTAAAGATCTCAATGATGATGATGATGATGATGATGATG 970
DB 1401 TACTGAAGACTGCTGCTGATCTTAAGATGCTCACTGATGATGATGATGATGATGATG 1460
OY 971 TAAGATTACAGTGTGATTAAGATGACAGTAAATTTGTAAGGATTCAGGAAGTTCA 1030
DB 1461 TAAACCACTGTTGATTAAGACATTAACAATTTGTAAGGATTCAGGATTCAGGATTC 1090
OY 1031 TATGCTAACGCTATTTGCACTGATTAATCCGATTTGAAACAACATTTGCTGATTTGA 1090
DB 1521 CATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
OY 1091 CCGTGAATAAATCTACAGAAAGCTTTGGCGAAATAGCTGCTGCTGCTGCTGCTGCTGCT 1150
DB 1581 CCGTGAATAAATCTACAGAAAGCTTTGGCGAAATAGCTGCTGCTGCTGCTGCTGCTGCT 1640
OY 1151 AGGAGCTCAACAGACAGCTTAAAGAAATGAAATCTGCTGCTGCTGCTGCTGCTGCT 1210
DB 1641 AGGAGCGCAACAGAAACGAACTTAAGCAATGAAATCTTATTAAGAGACGCACTTA 1700
OY 1211 TGTACACGCTGACAGCCGTTGAAGAGTATGTTGCTGCTGCTGCTGCTGCTGCTGCT 1270
DB 1701 TGAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
OY 1271 GGTATTTGAAAGTATGAGCTTGTGAGCTTGTGAGGATGATGATGATGATGATGATG 1330
DB 1761 TGGCATGCGAGCTTTGATTAATCTTCAAGAAAGGAGGATTAATCAACAGGAAATTA 1820
OY 1331 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1390

```

---

```

DB 1821 CGTTGCGCTGCCCTTTGAAAGACAGCTGCTGCAAAATCCGGCCAAATCAGAGATATGAAG 1880
OY 1391 CTCCTGATTTATGACAGATTTGAAAAACAGCCCTCAGAGAACAGATTTAATGCTCAAC 1450
DB 1881 TTCACCTTATTCATTTGATTAAGCTTCTGCAAAAAAAGTGTGATGATTAATGACGAC 1940
OY 1451 AGGTGAGGCTGATGATTAAGTAAACAGGATTCATGACCTGCTCAAGTAAACAGATC 1510
DB 1941 AGGTAAAGGCTAAATGATTTGATTAAGAGAAATCTTGACCCGCAAAAGTACTGCTTC 2000
OY 1511 AGCGTTAAATGACAGCTTCTGATGCTTATTTGTAACAAGACAGATTTGCTC 1570
DB 2001 AGCTTGAATAATGACAGCTTCTGCTGATTAATCTTGTACTGAAACAGTGTGTC 2060
OY 1571 TAAATAACCTGAACAGCTACGACAGC 1597
DB 2061 TAAATAACCAAGAACAGCTGCTGACAC 2087

```

---

```

RESULT 10
AB028452
LOCUS AB028452 2834 bp DNA BCT 07-DEC-1999
DEFINITION Bacillus sp. MS gene for Cpn10 and Cpn60, complete cds.
ACCESSION AB028452
VERSION AB028452.1 GI:6526959
KEYWORDS Cpn60; Cpn10.
SOURCE Bacillus sp. MS (strain:MS).
ORGANISM Bacillus sp. MS (strain:MS).
REFERENCE 1 (bases 1 to 2834)
AUTHORS Kondo,A. and Yoshida,M.
TITLE Cpn60/10 from Bacillus strain MS
JOURNAL Published Only in Database (1999) In press
REFERENCE 2 (bases 1 to 2834)
AUTHORS Kondo,A. and Yoshida,M.
JOURNAL Direct Submission
SUBMITTED (03-JUN-1999) to the DDBJ/EMBL/Genbank databases. Atsuko
Kondo, Kobe University, Department of Chemical Science and
Engineering, 1-1 Rokkodai-cho, Nada, Kobe, Hyogo 657-8501, Japan
(E-mail:kondocx.kobe-u.ac.jp, URL:http://www.kobe-u.ac.jp/,
tel:078-803-6196, fax:078-6206)
FEATURES
source
1..2834
/organism="Bacillus sp. MS"
/db_xref="MS"
/db_xref="taxon:96470"
534..818
/gene="Cpn10"
/gene="Cpn10"
/codon_start=1
/transl_table=11
/product="Cpn10"
protein_id="BA88109.1"
/db_xref="GI:6526960"
/transl_table="MkPDRVIVIEVTEBKASGIVLPDAKEKPOGRVAVGK
GRVLDSEKVAPEVEVGRDRIEFSKAGTEVYDKEYLLRESDLAVIG"
901..2520
/gene="Cpn60"
/gene="Cpn60"
901..2520
/codon_start=1
/gene="Cpn60"
/product="Cpn60"
/protein_id="BA88110.1"
/transl_table=11
/transl_table=11
/db_xref="GI:6526961"
/transl_table="MAKEIFSEEARLRVLDKADAVKTVLGPGRNVLEKFFG
SPLTNDGVTIAKEIILEDPEFENMGAKLVAIVASKTNDVAGDSTTAATVLAQAMIREG
LKNVTAGANMGVIRKIGIEKAVAVAEELKAIKSPKESIAOVAIISADEVGOLI
AEMERVGNDGVITLESGETTELDVEGQPDGKGVSPYMTDTEKNEVLEKPYI
LITDOKISNODILPILBOYVOGGRPLIINADIIEGALNLTIVNKLROGTFNAVVA

```

PGGDRRRKALMEDIAILLTGEFVISEELRELFKATIASIGRASKVVVTKENTTIVDGA  
 GDSERKRIINIOIRAOLEETSEEDREKREIAXIGARVYIKGATTELEKRL  
 RIEDLALNSRAAREGIVAGGCTALMNVKVAITAEDEDEKXILRIEPIVRO  
 IJONGESVYELKTERKGIOPNATKEMVDMLEAGIVPTVYTRSAJONASVA  
 AHELTTEAVVADKEPEENKGNKRPDGMH"

BASE COUNT 954 a 525 c 668 g 687 t  
 ORIGIN ,

Query Match 50.6% Score 840.4; DB 1; Length 2834;

Best Local Similarity 71.0% Pred. No. 1.2e-158;  
 Matches 1114; Conservative 0; Mismatches 456; Indels 0; Gaps 0;

QY 14 TATGCAAAAGAAATTAATTTTCAGCAGATGCGGCTGCTCCATGTCGCGGCAATGCA 73  
 DB 900 TATGCAAAAGAAATTAATTTTCAGCAGATGCGGCTGCTCCATGTCGCGGCAATGCA 959  
 QY 74 TATGTCAGATACCGTCATAAGTACGCTTGTCTTAAAGGGGCGCAATGTTCTTGA 133  
 DB 960 CAATTCAGTCAGATACCGTCATAAGTACGCTTGTCTTAAAGGGGCGCAATGTTCTTGA 1019  
 QY 134 AAAAGCTTTGCTTCCCTTAATTAATGACGGGTAACCATGCTTAAAGCATGCA 193  
 DB 1020 GAAAAATTTGGGTTCCCTTAATTAATGACGGGTAACCATGCTTAAAGCATGCA 1079  
 QY 194 ATTGAAGATCATTTTGAATAACATGGAGCAAAATTTGCTCTGAAGTGGCTCTTAAAC 253  
 DB 1080 ATTGAAGATCATTTTGAATAACATGGAGCAAAATTTGCTCTGAAGTGGCTCTTAAAC 1139  
 QY 254 CAAATGATATTCCTGCTGATGAGCAGCATCTGCAACAGTTTGAACACCAATGCTTCA 313  
 DB 1140 AAGCAGATGCTGCTGCTGATGAGCAGCATCTGCAACAGTTTGAACACCAATGCTTCA 1199  
 QY 314 TGAAGCACTAAATAATGATGACAGCAGTGTATATCAATGCTGCTGAGGCAATGGA 373  
 DB 1200 CGAAGATGCAATAATGATGACAGCAGTGTATATCAATGCTGCTGAGGCAATGGA 1259  
 QY 374 AAGCAGCAACGCAACAGCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA 433  
 DB 1260 AAGCAGCAACGCAACAGCTTGAAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA 1319  
 QY 434 GGAAGCTATTTGCTCAGGCTGCTGAGTATCATCAGCTTGAAGCCTTGAAGCCTTGA 493  
 DB 1320 AGAATCATGCTGCTCAGGCTGCTGAGTATCATCAGCTTGAAGCCTTGAAGCCTTGA 1379  
 QY 494 CTGAGCAAGTATGAGCCTGCTGAGTATCATCAGCTTGAAGCCTTGAAGCCTTGA 553  
 DB 1380 CGCAGCAAGTATGAGCCTGCTGAGTATCATCAGCTTGAAGCCTTGAAGCCTTGA 1439  
 QY 554 TATGCAAAAGAAATTAATTTTCAGCAGATGCGGCTGCTCCATGTCGCGGCAATGCA 613  
 DB 1440 TATGCAAAAGAAATTAATTTTCAGCAGATGCGGCTGCTCCATGTCGCGGCAATGCA 1499  
 QY 614 ATTCAGTGTACAGCAATGAATAATGCTGAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA 673  
 DB 1500 ATTCAGTGTACAGCAATGAATAATGCTGAGCCTTGAAGCCTTGAAGCCTTGAAGCCTTGA 1559  
 QY 674 CAGGATAAAAAGTGTCAAAACATCAAGACATTTTGCACATCTGAGGAAGTCTTAA 733  
 DB 1560 CAGGATAAAAAGTGTCAAAACATCAAGACATTTTGCACATCTGAGGAAGTCTTAA 1619  
 QY 734 AACCAACCGCTCATCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793  
 DB 1620 AACCAACCGCTCATCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1679  
 QY 794 TGTCTGACACAGATTCGCTGATCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853  
 DB 1680 TGTCTGACACAGATTCGCTGATCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739  
 QY 854 TGATCGTGTAAAGCTATGCTGTAAGACATGCTATCTGACAGGTGATGATGATGATGATGAT 913  
 DB 1740 TGATCGTGTAAAGCTATGCTGTAAGACATGCTATCTGACAGGTGATGATGATGATGATGAT 1799

QY 914 AGAGCTCTAGACCTGATTAAGATGCTACAAATGACAGCCCTTGACAGCTGCTAA 973  
 DB 1800 CGAAGACCTAGACCTGATTAAGATGCTACAAATGACAGCCCTTGACAGCTGCTAA 1859  
 QY 974 GATTCAGTTGATTAAGATGACAGCTGATTAAGATGCTACAAATGACAGCTGCTAA 1033  
 DB 1860 GATTCAGTTGATTAAGATGACAGCTGATTAAGATGCTACAAATGACAGCTGCTAA 1919  
 QY 1034 TGCTAACGTTATGACCTATTAATTCGATTTGAAGACACAACTTCTGACTTGAACG 1093  
 DB 1920 TAAAGCTGATTAACCAATTCGCTGCTATTAAGACACAACTTCTGACTTGAACG 1979  
 QY 1094 TGAATACTCAAGAAAGCTTTGCGCAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1153  
 DB 1980 TGAATACTCAAGAAAGCTTTGCGCAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2039  
 QY 1154 AGCTCAAGACAGACAGCTTTAAAGAAATGAATTCGCTGATGAGGATGCTTAAATG 1213  
 DB 2040 TGCAGCTACAGAAACAGATTTGAAGAAAGCAATTTACGATGAGAGAGCGCTACATC 2099  
 QY 1214 TACAGCTACAGCCGTTGAAGAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1273  
 DB 2100 TACAGCTACAGCCGTTGAAGAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2159  
 QY 1274 TATGAAAGATGACAGCTTGAAGAGATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1333  
 DB 2160 ATACAAATTAAGTTGCTGCTGATTAAGAGAGATGCTGCTGTGTGTGTGTGTGTGTGTGT 2219  
 QY 1334 GCTTCGCTGCTTGAAGAGACCTGTAACCTGTAATGCTTAAATGCTGCTGTAAGAGCTC 1393  
 DB 2220 TCTTCGCGCATTTGAAGAGACCTGTAACCTGTAATGCTTAAATGCTGCTGTAAGAGCTC 2279  
 QY 1394 CGTATGATTAAGATGTAAGAAACAGCCCTGACAGAAAGATTAATGCTGTAAGAG 1453  
 DB 2280 TGTCTATGTTGAAGCTTTAAAGAAACAGCCCTGACAGAAAGATTAATGCTGTAAGAG 2339  
 QY 1454 TGAGTGGCTGATGATTAAGAAACAGCTTGAACCTGTAATGCTGTAAGAGATGAC 1513  
 DB 2340 TGAATGGCTGATGATTAAGAAACAGCTTGAACCTGTAATGCTGTAAGAGATGAC 2399  
 QY 1514 GCTTCAAATGACCTGCTGTAAGCTGTAATGCTGTAATGCTGTAATGCTGTAATGCTGTA 1573  
 DB 2400 ACTTCAAAAGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2459  
 QY 1574 TAAACTGAA 1583  
 DB 2460 CAAACGAA 2469

RESULT 11  
 BACSGROESL 2309 bp DNA BCT 22-FEB-2000  
 LOCUS Bacillus stearothermophilus GroES (groES) and GroEL (groEL) genes,  
 complete cds.  
 DEFINITION  
 ACCESSION L10132  
 VERSION L10132.1 GI:289298  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCES  
 1. Schen, U. and Schumann, W.  
 Molecular cloning, sequencing and transcriptional analysis of the  
 groESL operon from Bacillus stearothermophilus  
 J. Bacteriol. 175, 2465-2469 (1993)  
 MEDLINE  
 FEATRES  
 93224474  
 Location/Qualifiers  
 1..2309  
 /organism="Bacillus stearothermophilus"  
 /strain="NUB36"  
 /db\_xref="taxon:1422"  
 249..533

gene

```
/gene="groES"  
249..533  
/gene="groES"  
/codon_start=1  
/transl_table=11  
/product="GroES"  
/protein_id="AAA22751.2"  
/db_xref="GI:7019626"  
/translation="MKPLGDRVIVIEVIEETEEKTAGIVLPDTAKERKPOEGRVAVVGK  
GRVLDSGERVADVEVEVDRIIFSKYAGTEVKYDKGEYLILRESDLIAVIG"  
606..2225  
/gene="groEL"  
606..2225  
/gene="groEL"  
/codon_start=1  
/transl_table=11  
/product="GroEL"  
/protein_id="AAA22752.1"  
/db_xref="GI:289300"  
/translation="MAKEIKFSEBARRAWLKGVDKLADAVKVLGPKGRVNVLEKKEG  
SPILTDGVTIAKELEDEPEENMGAKLVAEYASKTNDVADGDTTATVYLAQMTREG  
LKNVTAGANPMGIRKGTIEKAVAYAEIKAIKRPQCKEISAOYALSADEVGOLI  
AEAMERGVNDVITLESKFPATLVDVDSGMPDNGIVSPYITDTEKMEAVLENYI  
LITDKVSSIOEILILEQVYVQGRPLLIADVGEGLAVLVNKLKGFNVAVAKA  
PGGDRKRAMEDIALITGSEVISEELGHELSATIASLGRASVVTVENTTIVEGA  
GDSKRIRAKINQIRAOLEETSEDEKLEJERLALAGVAVIKVGAATTELKERL  
RIEDALNSTRAVEGIVAGGTAALMNVYSKVAALAEAGDEATGVKILRAIEEPYRQ  
IAOTAGLSEIIVERLKEKPGIGFNAAVTEGAVDIEAGIVDPKTVRSALQMAASVA  
AMELTEAVVADKPEENKGNPMPMGGM"  
BASE COUNT 771 a 430 c 553 g 555 t  
ORIGIN  
  
Query Match 50.5%; Score 838.8; DB 2; Length 2309;  
Best Local Similarity 70.9%; Pred. No. 2.5e-158;  
Matches 1113; Conservative 0; Mismatches 457; Indels 0; Gaps 0;  
  
QY 14 TATGGCAAAAGAAATCAATTTTCAGCATGCGCGTGCATCGCGAGTGA 73  
DB 605 TATGGCAAAAGAAATCAATTTTCAGCAAGAAAGCGCGATTTACGGGGTGA 664  
QY 74 TATGTAGCAGATACGCGTCAAGTACGCTGGCTCAAAAGGCCCATGTTGTTGA 133  
DB 665 TAACTAGCAGATGCGCTAAAGTACATTGGTCCAAAGGCCGTAACGTCGATTAGA 724  
QY 134 AAAAGCTTTGGTCTCCCTTAATTAAGTACAGGGGTACCATTCGTAAGAGATGA 193  
DB 725 GAAAATTTGGTCTCCCTTAATTAAGTACAGGGGTACCATTCGTAAGAGATGA 784  
QY 194 ATTAGAGATCATTTGAAAACATGGGAGCAAAATGGTGTGAAGGCGCTTAAC 253  
DB 785 ATTAGAGATCATTTGAAAACATGGGAGCAAAATGGTGTGAAGGCGCTTAAC 844  
QY 254 CAATGATTTGGTGTGATGAGGAGCTACTGCAACAGTTTGACACAAGCATTTCTCA 313  
DB 845 AAATGATTTGGTGTGATGAGGAGCTACTGCAACAGTTTGACACAAGCATTTCTCA 904  
QY 314 TGAAGACTAAAAAATGTGACAGAGTGTCAATCCATTTGATCGTCAGGACTGA 373  
DB 905 CGAAGATTTGAAAAAGTGTACAGCTGGCGCTAACCCAAAGGCGATCGTTAAAGTATTGA 964  
QY 374 AACAGCAACGCAACAGCTGTGAGCTTTGAAGCCATTTGCTCAACCTGTATCTGCA 433  
DB 965 AAAGGCGTGTGAGCTGTGAGGAGTAAAGCAATTTCCAAACCAATCAATCAAGTTAA 1024  
QY 434 GGAAGCTATTGCTCAGTGTGCTGCAATCATCATCCTGTGAAAAGTTGGAGATAT 493  
DB 1025 AGAATGATTTGCTCAAGTTGCAAGGATCTCTGGGTGACAAAGTTGGTCAATTAAT 1084  
QY 494 CTCGAAGCTATGAGGCGTGGGCAACGATGCTGATTTACATCGAAGATCTGAGG 553  
DB 1085 CGCAAGCAATGACGCGTTGGCAACGATGCTGATTTACATCGAAGATCTGAGG 1144
```

```
QY 554 TATGAAACGAACTTGAAGTGTGAAGCATGCAATTTGACCGTGTATACCTGTCA 613  
DB 1145 CTTCGCAACGGAATTAGATGTTGTCGAAAGTATGCAATTTGACCGTGTATGATCTCC 1204  
QY 614 ATACATGTCTACAGCAATGAAAAAATGTTGTCAGACCTGAAAACCCCTTATCTAAT 673  
DB 1205 ATACATGTCTACAGCAATGAAAAAATGAAAGCAAGTCTTGAATACTTACATCTTAA 1264  
QY 674 CAGGATTAATAAAGTGTCAAAATCAGCAAGCATTTTGGCAGTCTTGAGGAATCTTAA 733  
DB 1265 TACAGATTAATAAAGTGTCTACATTCAGAAATCTTGTCTATCTTGAACAAGTGTCA 1324  
QY 734 AACCAACGCTCATTAATCAATTAATGAGATGATGATGATGAGGAGCACTCCACCT 793  
DB 1325 ACAGAGAAACCGCTATTATTAATTCGGAAGATGTCGAAGGCGAAGGCTCGCAACAT 1384  
QY 794 TGTCTGAACCAAGTTCGTGCTACTTCAATGTGTGCTGTCAAAGCCGACAGATTTGG 853  
DB 1385 AGTCGTCAACCAATCTGTTGATCAATTCAAATGCGGTAGCGGTAAAGCCCTGCTCGG 1444  
QY 854 TGAATGCTGTAAGCTATGCTGAAGCATTTGCTATCTTACAGAGTGTGATGATTAC 913  
DB 1445 CGATCTGCTAAAGCGATGCTGAAGATATCCGATTTTAAGTGGCGTGAAGTATCTC 1504  
QY 914 AGAGATCTAGACATTTGAATTAAGATGCTACAAAGAGCCCTGACAGCGTGTAA 973  
DB 1505 CGAAGACTAGACGCTGAATTAATTAATGCAACAAATTCATGCTTGGCGCGCTTGAA 1564  
QY 974 GATTACAGTTGATTAAGATGACAGATTAATTTGTAAGGTTGCAAGATTCAGAGCTAT 1033  
DB 1565 AGTAGTTGTAAGCAAGAAATACAAATTCGTAAGAGCGCTGCGCATTTTAACCAT 1624  
QY 1034 TGCTAACGTAATTCGATGATTAATTCGATTAAGAAACAAACAACTTGTGACTGACCG 1093  
DB 1625 TAAAGCTGATCAACCAATTCGCTGGCATATTGAAGAACTACTTGGATTCGACCG 1684  
QY 1094 TGAATACTGCAAAAGAGTGTGGCAATTTAGCTGTGTGATGCTGTTATCAAGTAA 1153  
DB 1685 CGAAATTAACAGAGAGCGCTGCAAAATTAAGTGGCGCGCTGAGGTAATCAAGTGA 1744  
QY 1154 ACCTCCAAAGAGACAGCTTTAAAGAAATGAACCTTGCAATTTGATGCTTAATGC 1213  
DB 1745 TCGGCGACAGAAACAGAAATTTGAAGAACGCAAAATTTGCGCATGGAAGCGGCTCAAC 1804  
QY 1214 TACAGTGCACGCTGTAAGAGATTCGTTGCTGTGTGTAACAGCACTTAATACGT 1273  
DB 1805 TACTGTGCGGCTGTGCAAGAAAGTATCGTACCGCGCGTGTACGCAATTAATGAACGT 1864  
QY 1274 TATTAAAGATGACAGCTCTTGAAGCTTGAGGCGATGATCTAGAGCTAATCTGT 1333  
DB 1865 ATACAGCAAAAGTGTCTCAATCGAAGCGGAAGCGACAACTGTGTGAAAATCGT 1924  
QY 1334 GCTTCGTCTGTAGAAAGAGCTGTAGTCAATTTGCTTAATGCTGTGGTAGAAGGCTC 1393  
DB 1925 TCTTCGCGCAATGCAAGAGCAATTTGCTCAATTCGCGAATCTGTTGGAAAGCTC 1984  
QY 1394 CGTAAATTATGACAAGTTGAAAAACGCGCTGACGAACAGATTTAATCTCAACAG 1453  
DB 1985 TATCATTTGTTGAACGTTTAAACAGAAAAACCTTGCAATCGCTTCAACCGCTCTCG 2044  
QY 1454 TGAGTGGTGTATGATGATTAACAGAGATCTTGAACCTGTCAATTAACAGATCAGC 1513  
DB 2045 TGAATGGGTAGACATGATTTGAAGCTGTATCGTAAACCAACAAATAATCTGTTCTG 2104  
QY 1514 GCTTCAAAATGAGAGCTTGTGTAGCTATGTTATTTTGCAACAGACAGCTTGTCTAA 1573  
DB 2105 ACTTCAAAAGAGAGCTTGTGTGTGCTATGTTCTTAACACTGAACAGATGTTGTCTGA 2164  
QY 1574 TAAACTGAA 1583  
DB 2165 CAAACGAA 2174
```





```

Db 1340 TACAGAGACCTAGATTAGACTAAAAACGCTACTGTGATCACTTGTGACAGCTTA 1399
Oy 971 TAGATTAAGTATTAAGATAGACAGTATTTGTAAAGTTCAGAAAGTTCAGAAC 1030
Db 1400 CAAAGTACTGTAACAAAGATGATACAAATCTTAAGAGACAGGCGATTCCACAA 1459
Oy 1031 TATTGCTAACGTAATGCTACTGATTAATCGCAATTAGAAACAACACTTCTGACTTGA 1090
Db 1460 AATTAGCGCTCGCTAAACCAATCCGTAATGAGAAAGAACTCTCTGAATTTGA 1519
Oy 1091 CGGTAAAACTACAGAAAGTGGCGAAATTTACTGCTGCTACTGCTTATCAAGT 1150
Db 1520 TAGAGAAAAATTACAAACGCTTACAAAGTTCAGAGTGTGAGTACGCTGTGTAAGT 1579
Oy 1151 AAGAGCTCCACAGACAGCTTTAAAGAAATGAACCTTGCAATGAGATGCTCTAA 1210
Db 1580 CGGCGCTCCAACTGAAACAGCTAAAGAAAGCTAAATTAAGTATGATGATGCACTTA 1639
Oy 1211 TGTACAGCTGACGCGTGAAGAGTATCGTGGTGGTGGTGGTGAACAGCACTTATAC 1270
Db 1640 CTCTACTGCGCCAGCTGTAGAAAGATGCTGAGTGTGATGATGATGATGATGATG 1699
Oy 1271 GGTATTGAAAAAGTACAGCTCTGCTGAGGCGGATGATGATGATGATGATGATG 1330
Db 1700 TATTACAAATTAAGTACAGCTTGAAGCAAGAGCGAGTGAAGAAACAGATATCAACAT 1759
Oy 1331 TGTGCTGCTGCTGTAGAAAGCTGTACGCTCAATTTGCTTAAATGCTGGTACGAAAG 1390
Db 1760 TGTGCTGCTGCTGTAGAAAGCTGTACGCTCAATTTGCTTAAATGCTGGTACGAAAG 1819
Oy 1391 CTGGGTATGATGACAGTGAAGAAACAGCCCTGCGAGCAAGATTAATGCTGCAAC 1450
Db 1820 TTGCGTTATGCTGAAACGCTGTGAACAGAAAGAGTGGTGGTGTGAAAGCAAGCAA 1879
Oy 1451 AGGTAGTGGGTGATGATTAATAACAGGAATCATTTGACCTGTCAAGTAAACAGATC 1510
Db 1880 CGGCGAATGGGTAAACATGATGATGATGATGATGATGATGATGATGATGATGATG 1939
Oy 1511 AGCGCTCAAAATGACAGCTTCTGTAGCTAGTCTTATTTTGAACAAGAGCAAGCTGTGC 1570
Db 1940 CGCTCTCAAAATGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1999
Oy 1571 TAAATTAACCTGAACAGCTACGCCAGCCGACG 1602
Db 2000 AGACAAACAGCAAGAAACGCCGACGACGTG 2031

RESULT 13
AF274871 1977 bp DNA BCT 02-JAN-2001
LOCUS Bacillus stearothermophilus groESL operon, partial sequence.
DEFINITION AF274871
ACCESSION AF274871
VERSION AF274871.1 GI:12006266
KEYWORDS
SOURCE
ORGANISM Bacillus stearothermophilus.
Bacillus stearothermophilus.
Bacteria: Firmicutes: Bacillus/Clostridium group:
Bacillus/staphylococcus group: Bacillus.
REFERENCE
1 (bases 1 to 1977)
Snayman, M., Gochikyan, A., Weigel, P. and Sakhyan, V.
Effect of thermostable chaperonins on synthesis of proteins in
vitro
JOURNAL Unpublished
AUTHORS Snayman, M.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-2000) Laboratory of Biocatalyse, FRE-CNRS230,
University of Nantes (France), 2 rue de la Houssiniere, Nantes
44322, France
FEATURES
source 1..1977
Location/Oualifiers
1..1977
/organism="Bacillus stearothermophilus"

```

```

/strain="ATCC31783"
/db_xref="taxon:1422"
/db_xref="ATCC:31783"
<1..1977
/gene="groESL operon"
<1..285
</gene>
<1..285
</gene>
/gene="groES"
/note="Chaperonin: participates in protein folding"
/codon_start=1
/transl_table=1
/product="GROES"
/protein_id="AAG44814.1"
/db_xref="GI:12006267"
/translation="VIRPLDGVIVIVETERTKNSGIVLPDTRKEKPOGKVVAVNG
GRVLDNGORVAVPEVVDRIIFSKVIGTEVKIDKEVILNRESDLIVIG"
343..348
RBS
/gene="groEL"
343..1977
/gene="groEL"
358..1977
CDS
/gene="groEL"
/note="Chaperonin: participates in protein folding"
/codon_start=1
/transl_table=1
/product="GROEL"
/protein_id="AAG44815.1"
/db_xref="GI:12006268"
/translation="MKKEIFSEEARRLRGVDLADAVKVLGPGRNVLEKRF
SPLTINDGVTIAKEIELEDFEPMGAKLVEVASTNDVAGDITATVLAOMAREG
LKNVTAGANPGLIKGIERKAVAAVELEKAIKIPLOGKESIYAQVAAISADEVGGLI
AAEMERVNDGVITLESKGFTELDVVGQFQDGAAPVMTIDREKMAVENYAI
LITDKKISNIODLPLIEVOVGKPLILIEDVGEFALATVNTLRCTGTAIVAKA
PGFDRKRLMEDIALITGGEVISEIPELKSSTIASLRASVYVYKENTYIEGA
GDSRIKAPINORAOLEBETSEFPEKIOERLAKLGAIVAKVGAETELKEKRL
RIEDALDSTRAVBEGLVAGGALANYSKVALEAGDEATGVIVLRALEEVQ
IAQVAGLEGVIVERLTERPEGIFNAATGEVNNIENGIVDPKTVRSALNAAVSA
AMFLTTEVAVVDKPEENKNGNMPDMGGM"
BASE COUNT 653 a 386 c 495 g 443 t
ORIGIN
Query Match 49.2% Score 816.4 DB 2: Length 1977:
Best Local Similarity 70.0% Pred. No. 86-154:
Matches 1099; Conservative 0; Mismatches 471; Indels 0; Gaps 0:
Oy 14 TATGCCAAAGAAATCAATTTTCAGCAGATGGCGCTGCTGCATGTCGCGGAGTTGA 73
Db 357 TATGCCAAAGAAATTAATTAATTCACGCAAGAACTCGCGCATGTCGCGGAGTTGA 416
Oy 74 TATGTAGCAGATACCGCAAGTAACGCTTGTGCTTAAGGGGCGCATGTTGTTCTGA 133
Db 417 CAAAGTACTGATGCAAGTAAGTAAGTCAAGTCCAAAGGCCCTTAACGTTGATTTAGA 476
Oy 134 AAAAGCTTTGGTCTCCCTTAATTAATGACGGGGTAACCATGCTTAAGAGATCGA 193
Db 477 GAAAAATTCGTTCTCCATTAATCACTAACGCGTGTACAAATCCGGAAGAAATCGA 536
Oy 194 ATTAGAATCATTTTGAAGAAATGAGCAAAATGTTGTGTGAAGTGGCTTAAAC 253
Db 537 ATTAGAAGCCCATTTGAAGAAATGAGTGGTGAAGCTGTTGTGAAGTGAAGCAAAAC 596
Oy 254 CAATGATATTCCTGCTGATGGAGACGACTACTGCAACAGTTTGACACAAGCATTTGCA 313
Db 597 GAACGATGTCGTGGAGCGTACACACAGCAGAGTCTTGGGCAAGCAATGATTCG 656
Oy 314 TGAAGACTAAATAATGTGACAGCAGTGTCTATCCAAATTTGTCGTGAGGCAATTGA 373
Db 657 CGAAGATTGAATAACCTTACAGCTGCGCAAAACCAATGGGAATCCGCAAGATTTGA 716
Oy 374 AACAGCAACAGCAACAGCTTGAACCTTGAAGCAATGCTCAACCTGATCTGCGCA 433

```

Db 717 AAAAGCATGTCGTAGCGGTAGAGATTTAAAGCAATCTCCAAACCAATCCAGAGAA 776  
 Oy 434 GGAAGCTATTTCTAGAGTCCGCTGCAGATATCATCCGCTCTGTAAGAGTGAAGATAT 493  
 Db 777 AGAATCGATCCGCAAGATTTCTGCGGCTGACAGAGATGATGCTGAATTAAT 836  
 Oy 494 CTCAGAGCTATGAGCGGTGGCAAGCATGCTGATTAATCATCGAAGATCTGAGG 553  
 Db 837 CGAGAGCAATGGAACGGGTGGCAAGCATGCTGATTAATCATCGAAGATGGAAG 896  
 Oy 554 TATGGAAGCAATGGAAGTGTGAAGCATGCTGATTAATCATCGAAGATGGAAG 613  
 Db 897 TTTCAACCAAGATGATGCTGCAAGATGCAATTTGACGCGGCTATGCTCC 956  
 Oy 614 ATACATGTCACAGATACGAGAAATGGAACAGTGTGTAATCATATATCTTAAT 1016  
 Db 957 ATACATGTCACAGATACGAGAAATGGAACAGTGTGTAATCATATATCTTAAT 1016  
 Oy 674 CACGAGTAAAAAGTGCACAAATCCAGACATTTGGCCTACTTGAAGAGTCTTAA 733  
 Db 1017 CACTGACAAAAAATCTCGAACAATTCAGACCTCTGCTATCTTGAACAAGTGTGTA 1076  
 Oy 734 AACCAACGCTCATTAATCTATTAATGACAGATGATGATGATGATGATGATGAT 793  
 Db 1077 ACAAGGCAACCAATGATTAATCATCCGGAAGACGTCGAAGGCAAGCGCTTCGACAT 1136  
 Oy 794 TGTCTGACAAAGTTCGAGTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 853  
 Db 1137 AGTGTGAACCAATTCGCGTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1196  
 Oy 854 TGATGCTGTAAGATTCGCTGTAAGACATTCCTATCTGACAGATGATGATGAT 913  
 Db 1197 TGATGCTGTAAGATTCGCTGTAAGACATTCCTATCTGACAGATGATGATGAT 1256  
 Oy 914 AGAGATCTAGAGATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 973  
 Db 1257 CGAAGATCTAGAGATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1316  
 Oy 974 GATTCAGATTCGCTGTAAGATTCCTATCTGACAGATGATGATGATGATGAT 1033  
 Db 1317 AGTGTGTAAGATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1376  
 Oy 1034 TGCTAACGCTATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1093  
 Db 1377 TAAAGCTGCTATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1436  
 Oy 1094 TGAAGATCTGCTATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1153  
 Db 1437 CGAAGATCTGCTATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1496  
 Oy 1154 AGCTCAACAGATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1213  
 Db 1497 TCGCGGCAAGATTCGCTGTAAGATTCCTATCTGACAGATGATGATGAT 1556  
 Oy 1214 TACACGCTGCTGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1273  
 Db 1557 TACTGCTGCTGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1616  
 Oy 1274 TATTTGAAAAAGTACGCTTTCGCTGTAAGATTCCTATCTGACAGAT 1333  
 Db 1617 ATATGCAAGATTCGCTGTAAGATTCCTATCTGACAGATTCCTATCTGACAGAT 1676  
 Oy 1334 GCTTCGCTGCTGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1393  
 Db 1677 TCTTCGCTGCTGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1736  
 Oy 1394 CGTATGATTCGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1453  
 Db 1737 TGTATGATTCGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1796  
 Oy 1454 TGAATGCTGCTGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1513  
 Db 1797 CGAATGCTGCTGCTGTAAGATTCGCTGTAAGATTCCTATCTGACAGAT 1856

Oy 1514 GCTTCAAATGCACTTCTGTAAGATTCCTATTTTGACAACAGAGAGTGTGCTAA 1573  
 Db 1857 TCTGCAAAACGCACTTCTGTAAGATTCCTATTTTGACAACAGAGAGTGTGCTAA 1916  
 Oy 1574 TAAACCTGAA 1583  
 Db 1917 CAACACGAA 1926  
 RESULT 14  
 BACROESTL 2400 bp DNA BCT 26-Apr-1993  
 LOCUS Bacillus subtilis heat shock protein (groEL and groES) genes,  
 DEFINITION complete cds.  
 ACCESSION M81132.1 GI:143025  
 VERSION M81132  
 KEYWORDS groEL gene; groES gene; heat shock protein.  
 ORGANISM Bacillus subtilis (strain W168) DNA.  
 Bacteria; Firmicutes; Bacillus/Clostridium group;  
 Bacillus/staphylococcus group; Bacillus.  
 1 (bases 1 to 2400)  
 Li, M. and Wong, S.-L.  
 Cloning and characterization of the groEL operon from Bacillus  
 subtilis  
 J. Bacteriol. 174, 3981-3992 (1992)  
 JOURNAL MEDLINE 92283733  
 FEATURES  
 source Location/Qualifiers  
 1..2400  
 /organism="Bacillus subtilis"  
 /strain="W168"  
 /db\_xref="taxon:1423"  
 253..289  
 /evidence="experimental"  
 253..258  
 276..282  
 /note="putative"  
 340..346  
 /gene="groES"  
 340..638  
 /gene="groES"  
 354..638  
 /gene="groES"  
 /standard\_name="groES (cpn10)"  
 /codon\_start=1  
 /transl\_table=1  
 /function="Molecular Chaperone"  
 /evidence="experimental"  
 /product="heat shock protein"  
 /protein\_id="AA02502.1"  
 /db\_xref="GI:143025"  
 /translation="MKPLDRLVITLVESEKTAASGIVLPDSKKEKPEQKIVAAAGS  
 GVLESGERVALEVKESDRITFSKTAGTEVKTEYLILRESDLAVIG"  
 669..675  
 /gene="groEL"  
 /evidence="experimental"  
 669..2319  
 /gene="groEL"  
 685..2319  
 /gene="groEL"  
 /standard\_name="groEL (cpn60)"  
 /codon\_start=1  
 /transl\_table=1  
 /function="Molecular Chaperone"  
 /product="heat shock protein"  
 /protein\_id="AA02503.1"  
 /db\_xref="GI:143027"  
 /translation="MAKEIKESPEARARALRGVALADAVYVTLGPKGNVLEKPKF  
 SPLINDGVTAKELIELEDAPEKMGAKIAYASSTNDVAGDGTATTAALAMIREG  
 LKNTAGANPVGKRGKREDAVAYIENLEKISKPIEGRESIAQYAAISADEVSGLI  
 AEMERGVNDVITLESKFTTELEVVGQFDPGRASPIVATSDDKMEAVLDNPI  
 LITDKKITINIOELIPYLEVOYQGRPLLIADVEGELATLVVNRILRGTFAVAVKA

Query Match	48.68;	Score 807.4;	DB 2;	Length 2400;
Best Local Similarity	68.08;	Pred. No. 5e-152;		
Matches 1126; Conservative	0;	Mismatches 531;	Indels 0;	Gaps 0;

QY	901	GTATGATGATTAACAGGATGATAGACCTGTAATTAAGAATGCTACAAATGACAGCCCTTG	960
Db	1571	GAGAAATGATACAGAAAGATCTTGCCCTTGACCTGAAATCTACTCAAATCGCTCAATGG	1630
QY	961	GACAGGCTGCTAAGATTACAGTTGATTAAGATAGCACAGTAATTTGTTGAAGGTTCAGAA	1020
Db	1631	GACCCGCTTCTAAGATTGCTGTACTAAAGAAAACACAAATCTGTGAAGCGCGTGGG	1690
QY	1021	GTTGACAGAGCTAATGCTTAACCGTATGACATGATTAANTGCAATTAAGAAACAACTT	1080
Db	1691	AAACAGCAAAATTTTGCTTGCCCTGTGACATCAATCCGCGCTCAAGTGGAAAGAACTT	1750
QY	1081	CTGACTTTGACCGTGAAAAATCTACAGAAGCTTTGGCGAAATTAAGCTGTGATAGCTG	1140
Db	1751	CTGAAATTCGACAGAAAAAATTAACAGAGCCCTTCTGTAACCTGCTGGCGCGCTAGCTG	1810
QY	1141	TTATCAAGATAGAGCTCCACAGACAGACGTTTAAAGAAATGAATCACTTCATAGAG	1200
Db	1811	TCATCAAGATGCGCGCTGCGATGAAATGAGCTGAAAGAGCTTAATCTCCATCGAAG	1870
QY	1201	ATGCTCTAAATGCTACAGCTGACGCGCTTGAAGAAGTATCGTTGCTGCTGCTGSAACAG	1260
Db	1871	ACGCTTGAACTCAATCGCGAGCTGTTGAAGAAGCAATCGATCCGGTGTGTGATACG	1930
QY	1261	CACCTATTACGGTATTATGAAAAAGTAGACGCTCTTGAGCTTGAGGCGCATGATGCTACTG	1320
Db	1931	CGCTTGTAACCTATATAFAACAAAGCGCTGAGTGAAGCTGAAGGCGATGCTCAAG	1990
QY	1321	GAGCTAAATGCTGCTGCTGCTCTAFAAAGAGCTGTAGCTCAATTTGCTTTAAATGCTG	1380
Db	1991	GTTCAACATCTGCTGCTGCGCTGTAAGAAGCAATCGCTCAATTCGACACAAAGCTG	2050
QY	1381	GGTAGCAAGGCTCCGTAAGTTATGACAAAGTTGAAAAACAGCCCTGCAGAGAACGATTTA	1440
Db	2051	GCTTTAAGAGATCTGATCTGTTAGAGGCCCTCAAAAAAGAAATCGGCGTAGGCTTCA	2110
QY	1441	ATCTCCACAGCAGTAGAGGGTGTATTAATTAAGAAAGAAATCAATGACCTGTGCAAG	1500
Db	2111	ACGCTGCACATCGCAATAGGCTTAACATGATCGAAAAAGATGCTTGACCCAAACAAAG	2170
QY	1501	TAAACGATCAGCGCTTCAAAATGACAGCTTCTGTAGCTAGTCTTAATTTGACACAGAG	1560
Db	2171	TTACAGGCTCACCTCTTTCAAAACCTCGCTGTAGCTCAATGTTCTTAACACAGAG	2230
QY	1561	CAGTTTGTCTTAATTAACCTGAACAGCAGCTACGCGACAGCAGCATGCGACAGTATGG	1620
Db	2231	CTGTGTGCTGACAAAGCCAGAAAGAAACAGTGGCGCGCCAGAGATGCTGATATGGCG	2290
QY	1621	ATCCAGGATGATGGGTGGGATGGGCGGATACCCCA	1657
Db	2291	GCATGGGCGGATGGGTGATGATGTAATAAAGGA	2327

RESULT 15

BACHSPA

LOCUS

DEFINITION B subtilis groES and groEL genes, complete cds.

ACCESSION M84965.1

VERSION GI:143061

KEYWORDS ATPase; chaperonin protein; heat shock protein.

SOURCE Bacillus subtilis (strain MB1) DNA.

ORGANISM Bacillus subtilis

REFERENCE 1 (bases 1 to 2525)

AUTHORS Schmidt A., Schleesswohl M., Voelker U., Hecker M. and Schumann W.

TITLE Cloning, sequencing, mapping and transcriptional analysis of the groES operon from Bacillus subtilis

JOURNAL J Bacteriol. 174, 3993-3999 (1992)

MEDLINE 92283754

FEATURES

Location/Qualifiers

1..2525

2525 bp DNA

BCP

26-APR-1993

gene /strain="MB11"  
/db\_xref="taxon:1423"  
168..452  
/gene="groES"  
168..452  
/gene="groES"  
/codon\_start=1  
/product="heat shock protein"  
/protein\_id="AA22530.1"  
/db\_xref="GI:143062"  
/translation="MLKPLGDRVIELEVESEKTAAGTLPDSAKKEPOEGKIVAAAGS  
GRVLESEGERVALEVEGRDIIIFSKVAGEVKEETELLILRESDIILAVIG"  
499..2133  
/gene="groEL"  
499..2133  
/gene="groEL"  
/codon\_start=1  
/translation="11  
/product="heat shock protein"  
/protein\_id="AA22531.1"  
/db\_xref="GI:143063"  
/translation="MAKEIKFSEBARMLRGVADALADAVKVLGPKGRNVYLEKRG.  
SPLITNDGYIAKEIELEDAFENKGAIVAEVASKTNDVAGDGTATATLAQAMREG  
LKNTVAGNPVGRKMEQAVAIENLKEISRKESIAQOVAISADDEPGLI  
AEMERVNDGYITTEESKGTTELVEVEEDPDRGASPYWTDSDKREAVLNDPYI  
LITDKITIMORILPVEQVVOCKPILLIAEDVEGALATLVYKRLKGTMAVAVKA  
PGSGDRKAMLEDAIVLTGEVITTEDLDLSTQIADGSRKVTREKNTVEGA  
GETDKISAKVTVIAQVEITSEFDRELDKRLAGAAVAVKVAATLELLEKRL  
RIDALNSTRAVEGIVSGGTALVYVYKVAVEADGATGIVLIRALEPILRO  
IINAGLESGVIERLKNKEIEIGVFNATGEMVNIEMKGIYDPTKVTLSALONASVA  
AMFLTTEAVVADPEENGSGAMPDMNGMNGMGM"

BASE COUNT 781 a 504 c 603 g 637 t  
ORIGIN

Query Match 48.68; Score 807.4; DB 2; Length 2525;

Best Local Similarity 68.08; Pred. No. 4.9e-152;

Matches 1126; Conservative 0; Mismatches 531; Indels 0; Gaps 0;

QY 1 GAATTCGGCTCATATGCGCAAAAGAAATCAATTTTCAGCAGATGCCGCTGCCTCATGG 60  
DB 485 GAGGCTCTGTAAACATGGCAAAAGAAATTAAGTTAGTGAAGAAAGCTCGCGGCAATGC 544  
QY 61 TGGCGGAGTGTATGATGTAGCAGATACGTCAGTACGCTGTGCTTAAAGGCGCA 120  
DB 545 TTGCGGAGTGTATGATGTAGCAGATACGTCAGTACGCTGTGCTTAAAGGCGCA 604  
QY 121 ATGTGTTCTTGAAGAAAGCTTTGTTGCTTCCCTTAATTACTAATGACGGGTAACATTG 180  
DB 605 ACGTGGCTTGAAGAAAGCTTTGTTGCTTCCCTTAATTACTAATGACGGGTAACATTG 664  
QY 181 CTAAAGAGATGAAATTAAGATCATTTTGAAGAAACATGGAGCAAAATTTGCTGGAAG 240  
DB 665 CTAAAGAGATGAAATTAAGATCATTTTGAAGAAACATGGAGCAAAATTTGCTGGAAG 724  
QY 241 TGGCTTCTTGAAGAAAGCTTTGTTGCTTCCCTTAATTACTAATGACGGGTAACATTG 300  
DB 725 TAGCCAGCAAAAGAGAGCTTGGCGGTGAGCAACAAACGCAACAACTCTTGGCC 784  
QY 301 AAGCCATTGTCATGAGAGCACTAAAGATGTACAGCAGTGTATCAATTCATTTGATCC 360  
DB 785 AAGCCATTGTCATGAGAGCACTAAAGATGTACAGCAGTGTATCAATTCATTTGATCC 844  
QY 361 GTCGAGCATTTGAAGCAAGCAAGCAGTGTGAAGCTTAAAGCATTTGCTCAAC 420  
DB 845 GTAAAGGATGGAACCAAGCTGTAGCGTTGCGATGAAATTTAAAGAAATTTCTTAAC 904  
QY 421 CTGATCTGCAAGGAGATTTGCTCAGTGTGCTGCAATCATCAAGCTCGTGAAGAG 480  
DB 905 CAATCGAAGCAAGAGATCTATGCTCAGTGTGCTGCAATCATCAAGCTCGTGAAGAG 964  
QY 481 TTGAGAGATATCTCAAGAGCATGTAGAGCGGTGCGCAACGATGGTGTATTCACATCG 540

DB 965 TCGGAAGCCTTATGCTGAAGCAATGAGACCGCTGAGNAACGAGCGCTTATCAATC 11  
QY 541 AAGAACTCTGAGGATGTAAGCAAGCACTGAAGTGGTGAAGGCATGATTTGACCGG 11  
DB 1025 AAGACTCTAAGGCTTCAACACTGACCTGGAAGTGTGAAGGATGATTCAGACCGG 11  
QY 601 GTTACCTCTCAATFACATGCTACAGACATGAAAAATGCTGACAGCTTGAAMAC 660  
DB 1085 GATAGCGCTCTCTTACATGTAAGTACGACTGATTAAGTGAAGCGCTTCTCAATC 1144  
QY 661 CATTTATCTATACGAGATTAAGTCAACATCAACATCAAGCATTTGCCACTAGT 720  
DB 1145 CTACATCTTATACAGACAAAAAATACAAACATTCACAGAAATCTCTGCTGCTG 1204  
QY 721 AAGAGTCTTAAACCAACCGCTCTCTCTATTCATTTATGACATGATGTGATGTAAG 780  
DB 1205 ACGAGGTTGTACAGCAAGCAACCATGCTTCTGATCGCTGAGAGATGTTGAAGCGAG 1264  
QY 781 CACTTCAACCCCTGTCTTGACACAGATTCGTGACTTCAATGTGTGCTGCAAG 840  
DB 1265 CACTTGTACACTTGTGTGAACAAACCTCGCGGACATCAACGAGTGGCTGTAAAG 1324  
QY 841 CGCCAGATTTGGTGAATCGCTGTAAGATGATGCTGTAAGACATTTGCTATCTGACAG 900  
DB 1325 CTCTCGTTTGGGATCGCGCTGTAAGCAATGCTTGAAGACATCGCTTCTACTGCG 1384  
QY 901 GTACAGTATTAACAGAGATCTAGACCTTGAATTAAGATGCTACATGACAGCCCTTG 960  
DB 1385 GAGAAGTATACACAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444  
QY 961 GACAGCGCTGATAGATAGTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1020  
DB 1445 GACGCGCTTCAAGTGTGCTTACTTAAAGAAACACACATCGTTGAAGCGCTGCG 1504  
QY 1021 GTTCAAGCTATTTGCTTAAACCGTATGCTATTAATGCAATTTGAACCAACATT 1080  
DB 1505 AAACGAGCAAAATTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1564  
QY 1081 CTGACTTTGACCGTGAAGAACTACAAAGAACTTTGGGGAATTTAGTGGTGTAGCTG 1140  
DB 1565 CTGATTCGACAGAGAAATTAACAAAGCGCTCTGCTAACTGCTGCGCGCTGAGCTG 1624  
QY 1141 TTATCAAGTACAGCTCCACAGACAGACCTTTAAAGAAATGAATCTCCATTGACG 1200  
DB 1625 TCATCAAGTACAGCTCCACAGACAGACCTTTAAAGAAATGAATCTCCATTGACG 1684  
QY 1201 ATGCTCTAAATGCTACAGCTGACAGCGCTTGAAGAGCTATGCTGCTGCTGTAACAG 1280  
DB 1685 ACGCTTGAACCTCACTCGCGAGCTGTGAAGAGCATGATCCGGTGTGTACAG 1744  
QY 1261 CACTTATTAAGGTTATTAAGAAAGTACAGCTGCTGAGCGCTGAGCGCTGATGCTAG 1320  
DB 1745 CGCTTGAACGATATTAACAAAGCTGCTGCAATGAGCTGAAAGCGCTGCTCAAGAG 1804  
QY 1321 GACGTAACATTTGCTTGTGCTGTAGAAGAGCTGTACGTAATTTGCTTAAATGCTG 1380  
DB 1805 GTATCAACATCGCTTCCGCGCTTGAAGAGCAATCCGTAATTCGCAACAGCTG 1864  
QY 1381 GGTAGCAAGGCTCGTATGTTATTAAGAAAGCAAGCCCTGCAAGAAAGATTTA 1440  
DB 1865 GCGTTGAAGATTTGTCATCGCTTGAAGCGCTCAAAAAGAAAGAAAGCGCTGAGCTTCA 1924  
QY 1441 ATGCTGACAGAGTGTGCTGTATGATTAAGAGATTAAGAGATTAAGAGATTAAG 1500  
DB 1925 ACGCTGACAGTGTGCTGTATGATTAAGAGATTAAGAGATTAAGAGATTAAGAG 1984  
QY 1501 TAAACAGTACAGGCTTCAAAATGACAGCTTCTGATGCTATTTATTTGACACAGAG 1560  
DB 1985 TTACAGCTCAGCTTCAAAAGCTGCTGCTGTAGCTGCAATGCTTCAACACAGAG 2044  
QY 1561 CAGTTGCTGCTTAAACCTGACAGCTACGCCAGCGCCAGCATGCTCCACAGATGAG 1620

Wed Nov 14 11:59:03 2001

us-09-001-737-7.rge

Page 22

Db 2045 CTGTTGTCCTACACAGCCAGAGAAAAAGGTGGCGCGCAGAGATGCTGATATGGCG 2104

Oy 1621 ATCCAGGATGATGGGTGGGATGGCGCGGATAGCCGA 1657

Db 2105 GCATGGCGGTATGGGTGGATGATGTATATAAGGA 2141

Search completed: November 9, 2001, 10:37:16  
Job time: 4418 sec ,